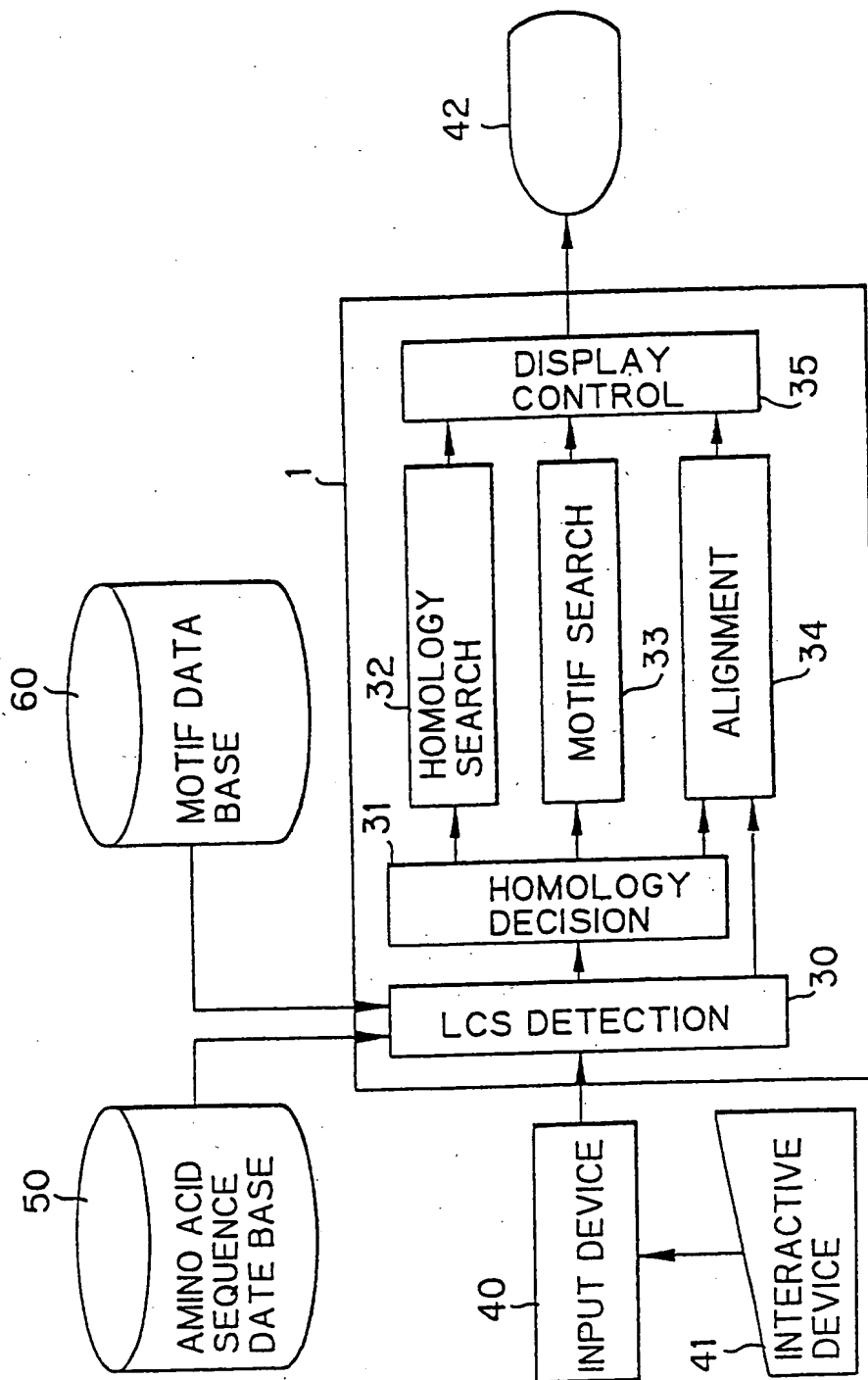
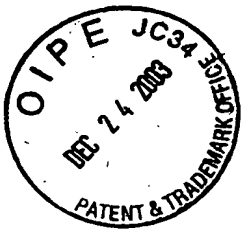




1/45

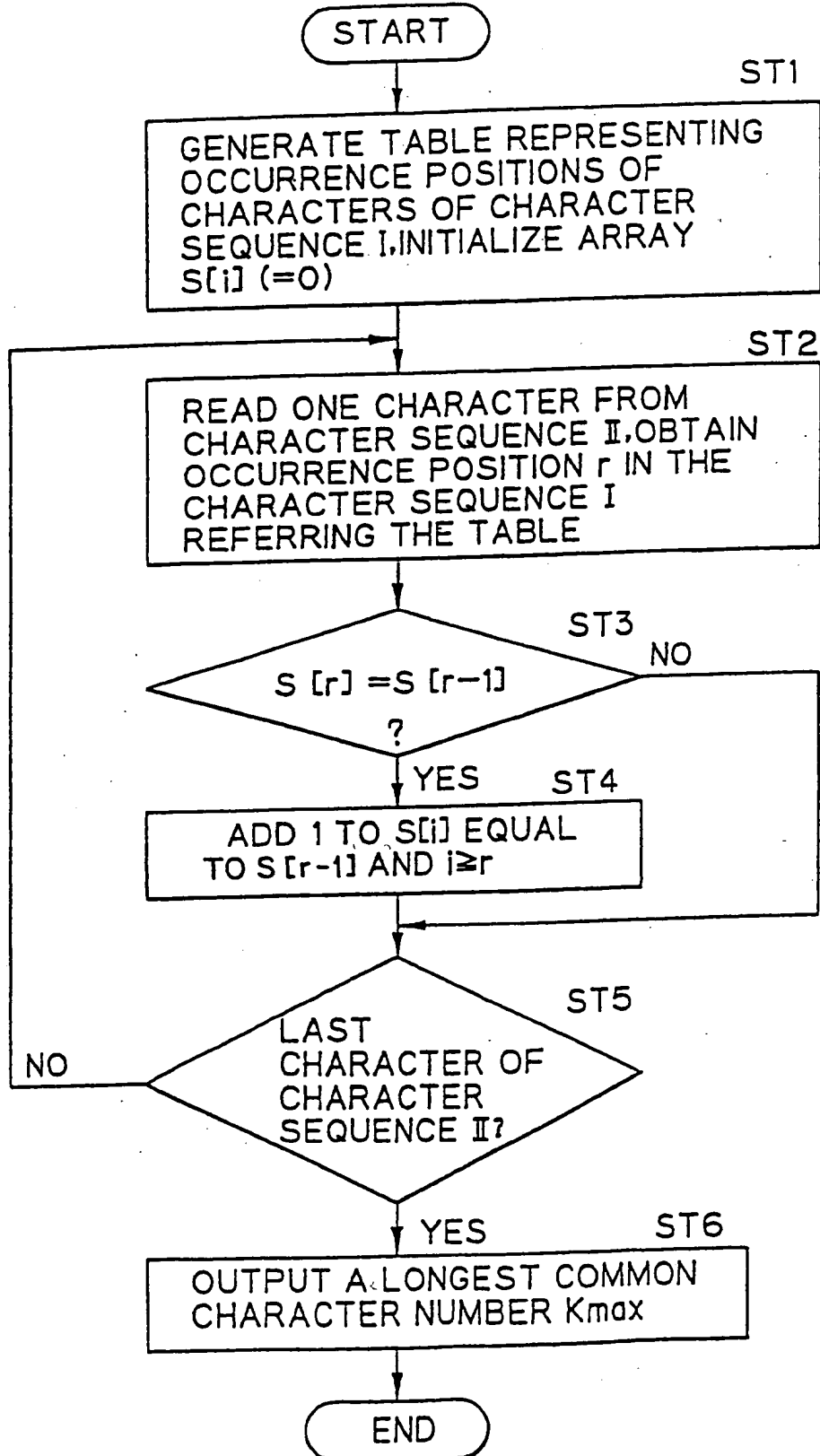
Fig. 1

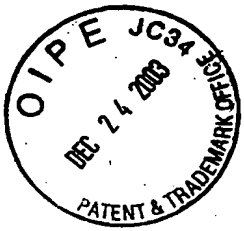




2/45

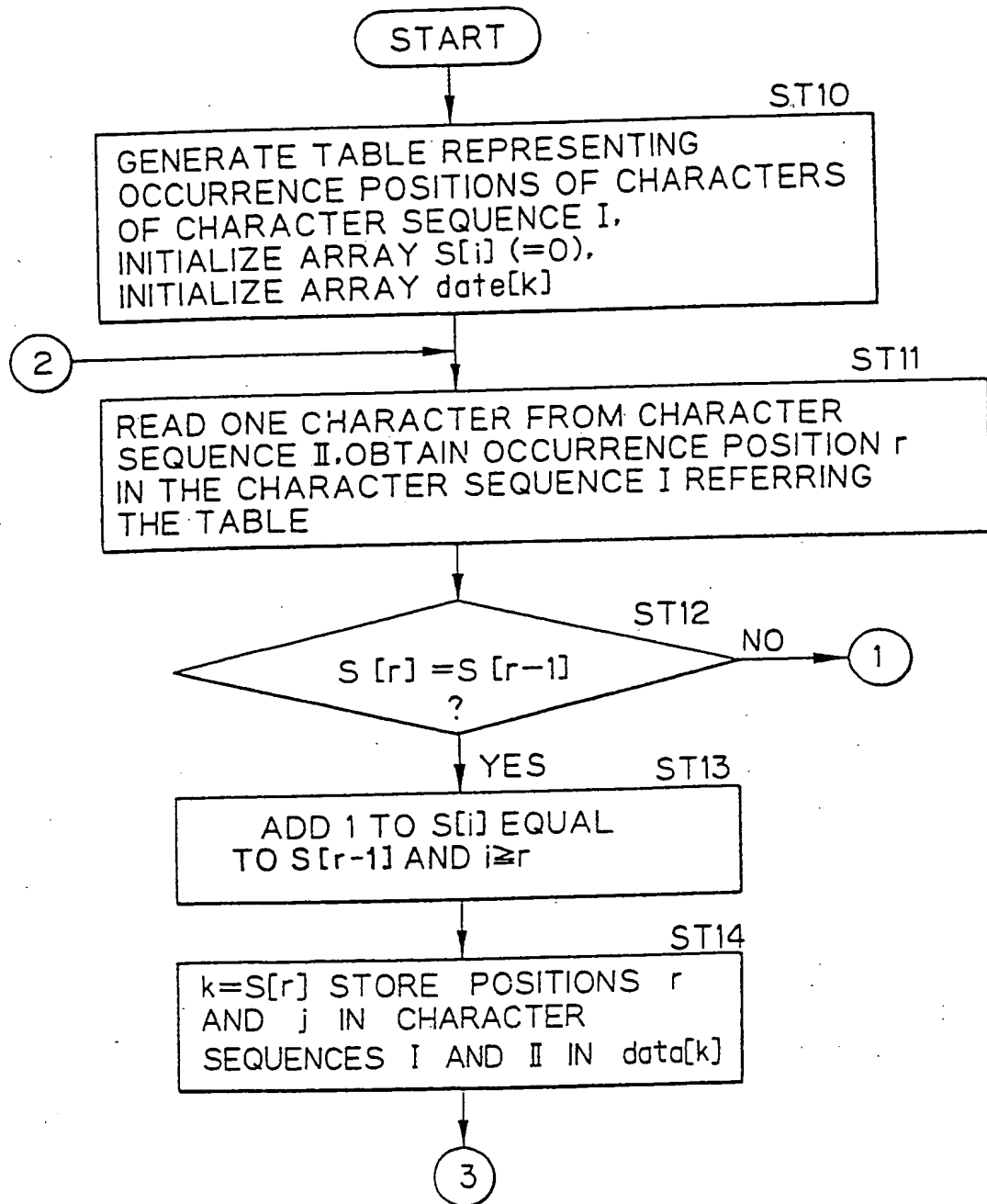
Fig. 2

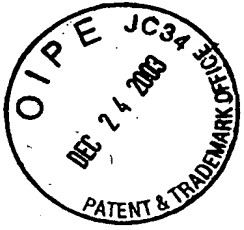




3/45

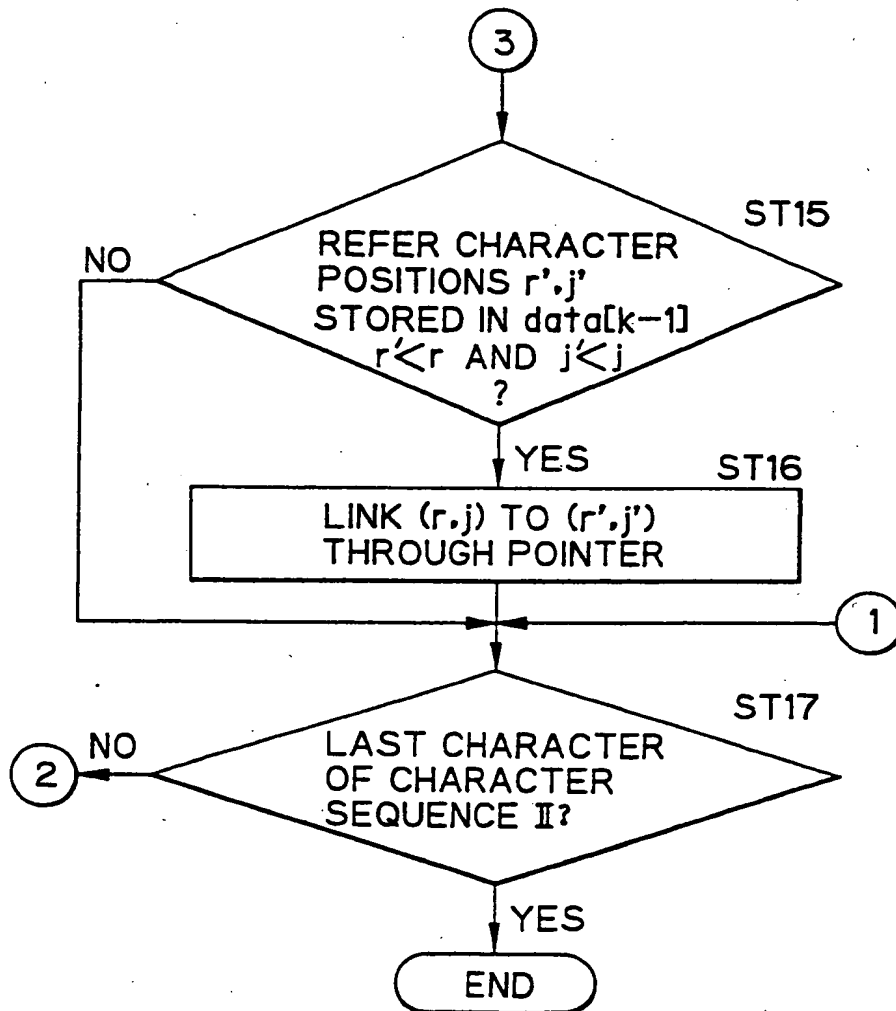
Fig. 3





4/45

Fig. 4



5/45



Fig. 5

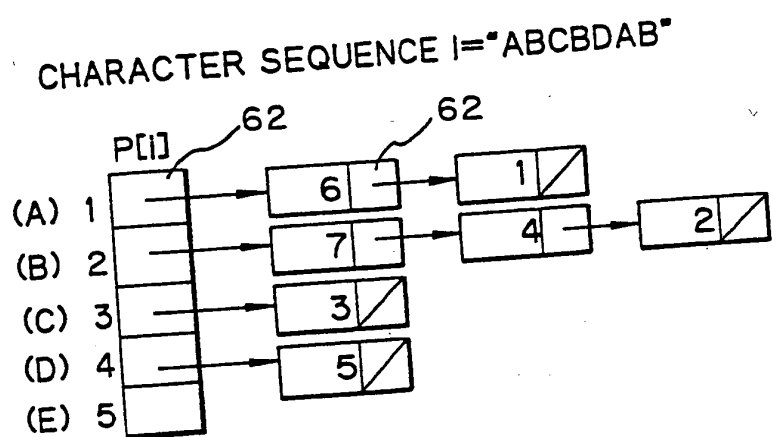




Fig. 6

CHARACTER SEQUENCE II = "BDCABA"

6/45

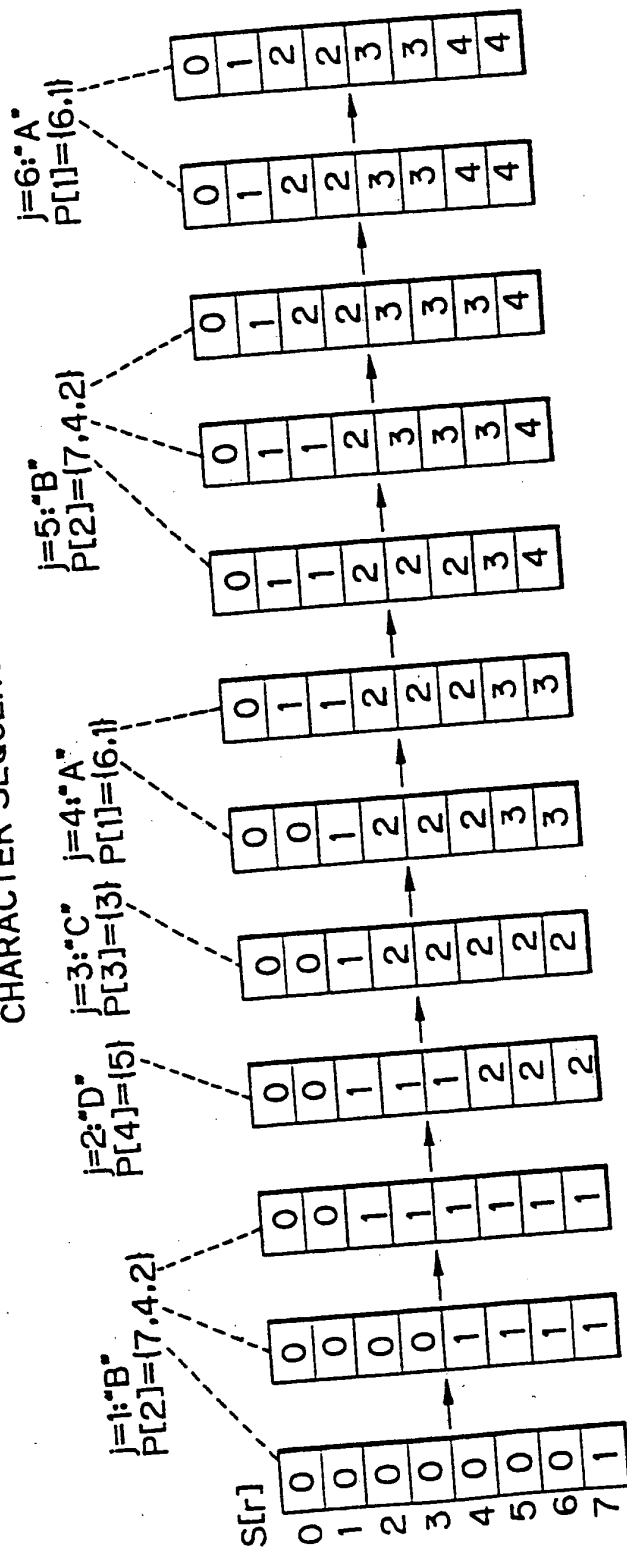
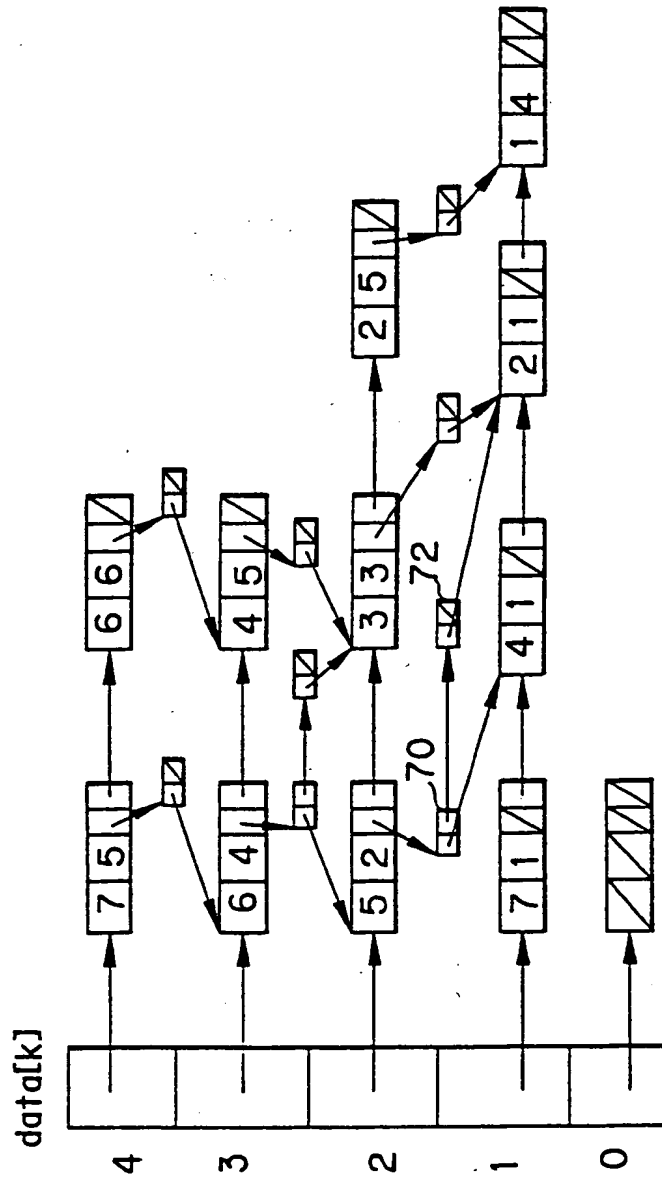
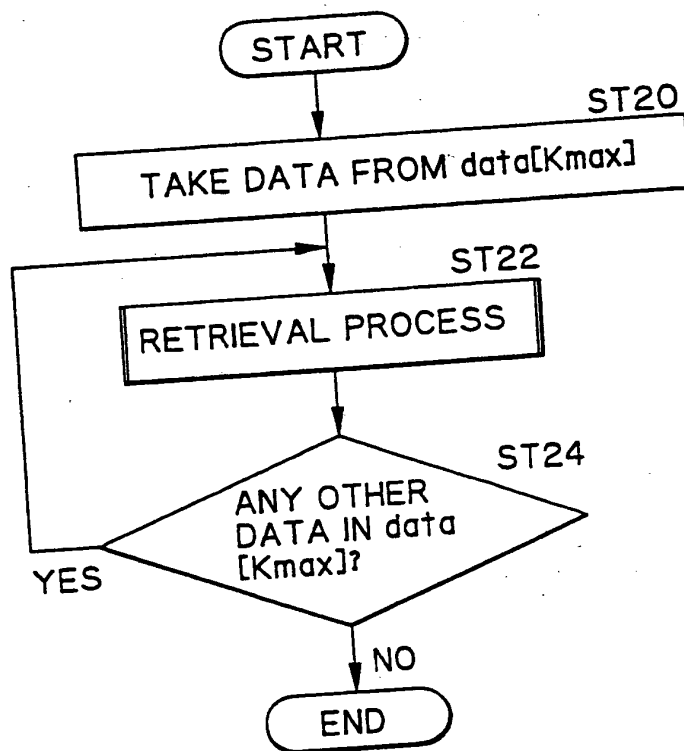




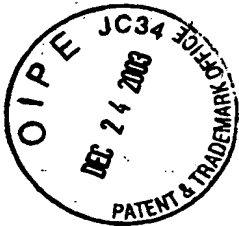
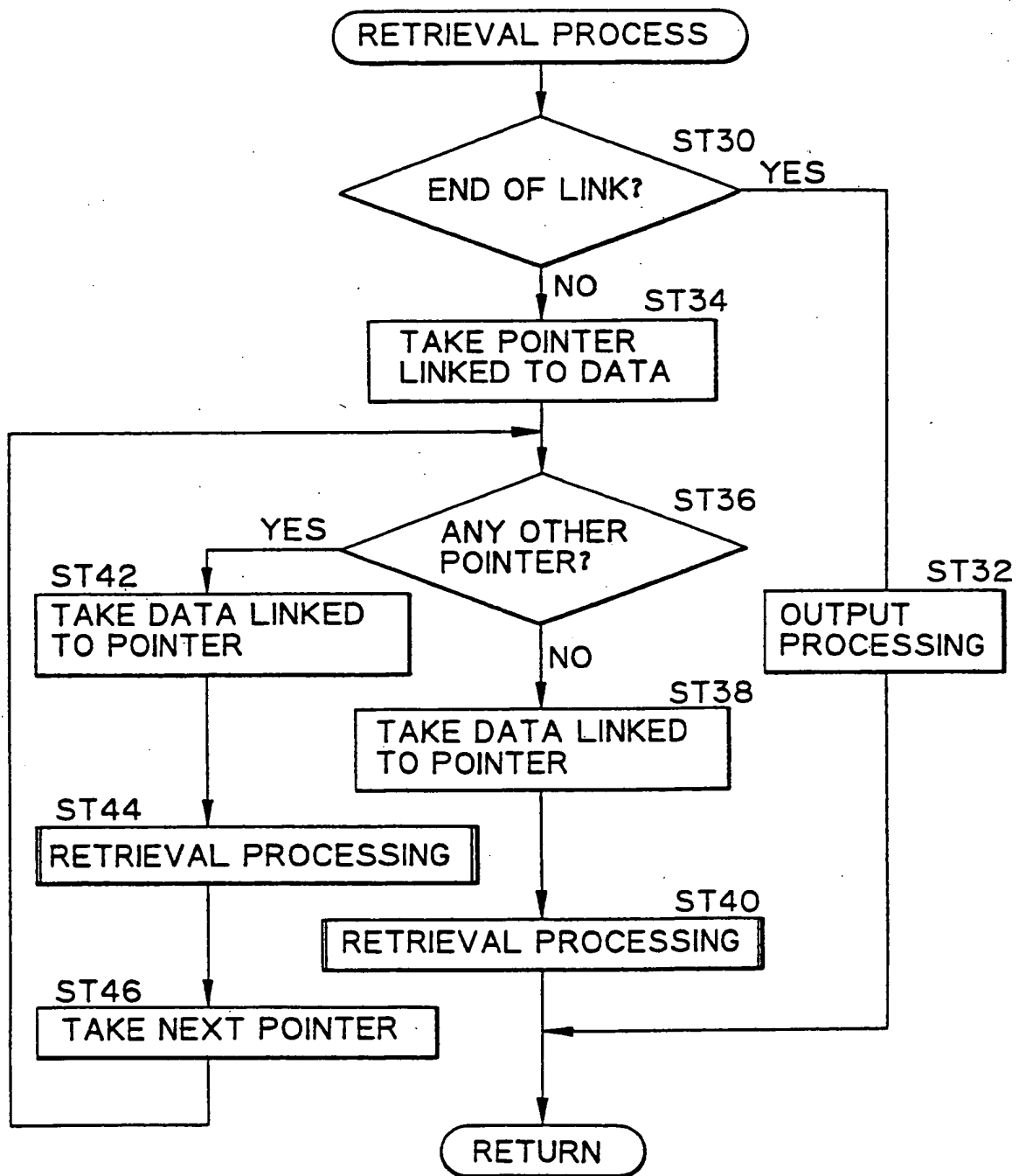
Fig. 7

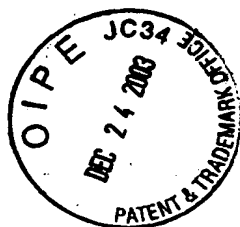


8/45

*Fig. 8*

9/45

*Fig. 9*



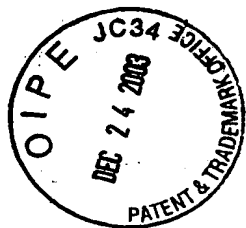
10/45

Fig. 10

human : GDVEKGKKIFIMKCSQCHTVEGGKHKTGPNLHGLFGRK SEQ ID NO: 1
 bacterium : EGDAAAGEKVSKCLACHTFDQGGANKVGPNNLFGVF SEQ ID NO: 2

LCS : GD(x3.3)G(x0.1)K(x0.2)K(x4.0)KC(x2.2)CHT(x3.3)GG(x2.2)K
 GD(x1.4)E(x0.2)K(x0.2)K(x0.4)KC(x2.2)CHT(x3.3)GG(x2.2)K

homology : 47%



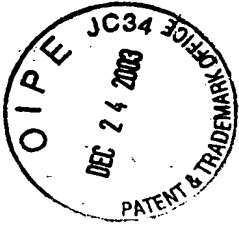
11/45

Fig. 11

Rat : MSLAILRVIRLVRVFRIFKLSRHSKGLQILGRTLKASMRELGLLFFIGVV

leucinzip. L(6)L(6)L(6)L(6)L

SEQ ID NO: 3

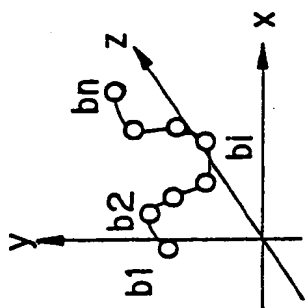


12/45

Fig. 12

human : GDVEK G K KIFIMKCSOCHTVEKGG KHKTGPNLHGLFGRK ... SEQ ID NO: 1
bacterium : E GDAAAGEKVK KCLACHTFDQGGANKV GPNPN LFGVF ... SEQ ID NO: 2

Fig. 13 B



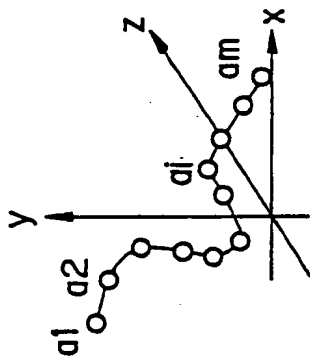
$$B = \{b_1, b_2, \dots, b_j, \dots, b_n\}$$

Fig. 13 D

$$r.m.s.d = \sqrt{\frac{\sum_{k=1}^n w_k (U b_k - a_k)^2}{n}}$$

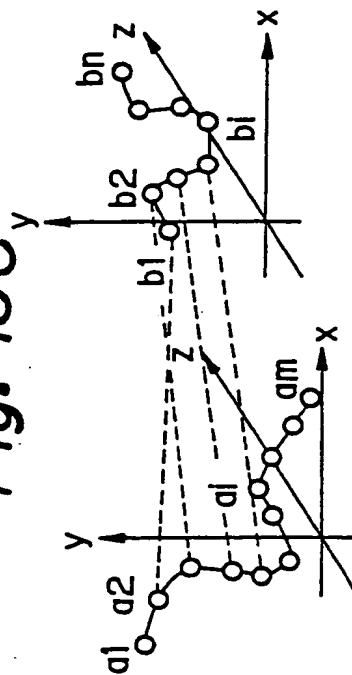


Fig. 13 A



$$A = \{a_1, a_2, \dots, a_i, \dots, a_m\}$$

Fig. 13 C



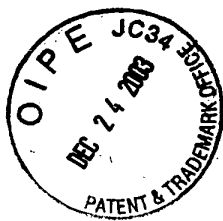


Fig. 14 A

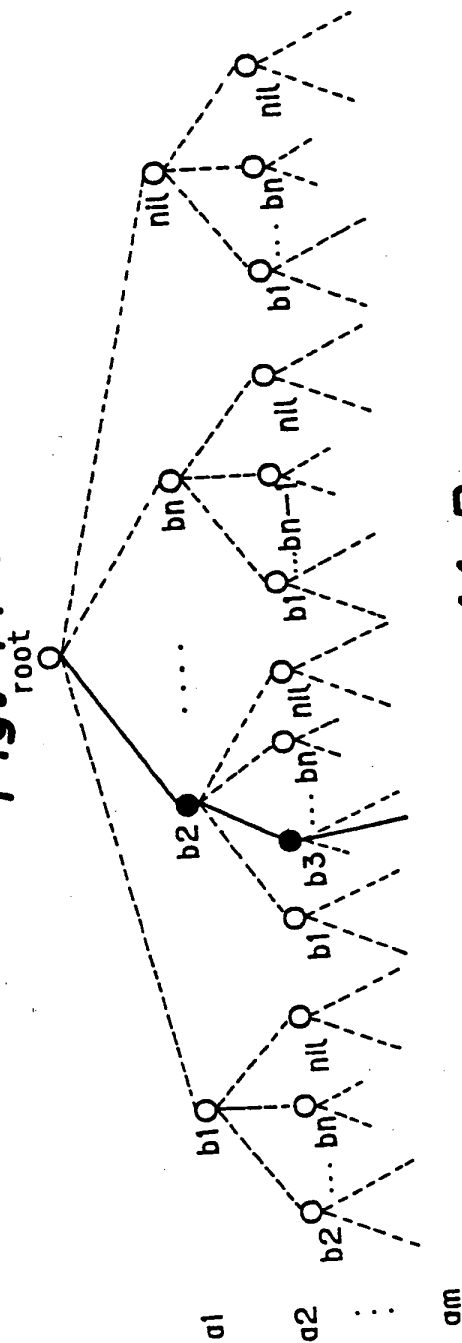
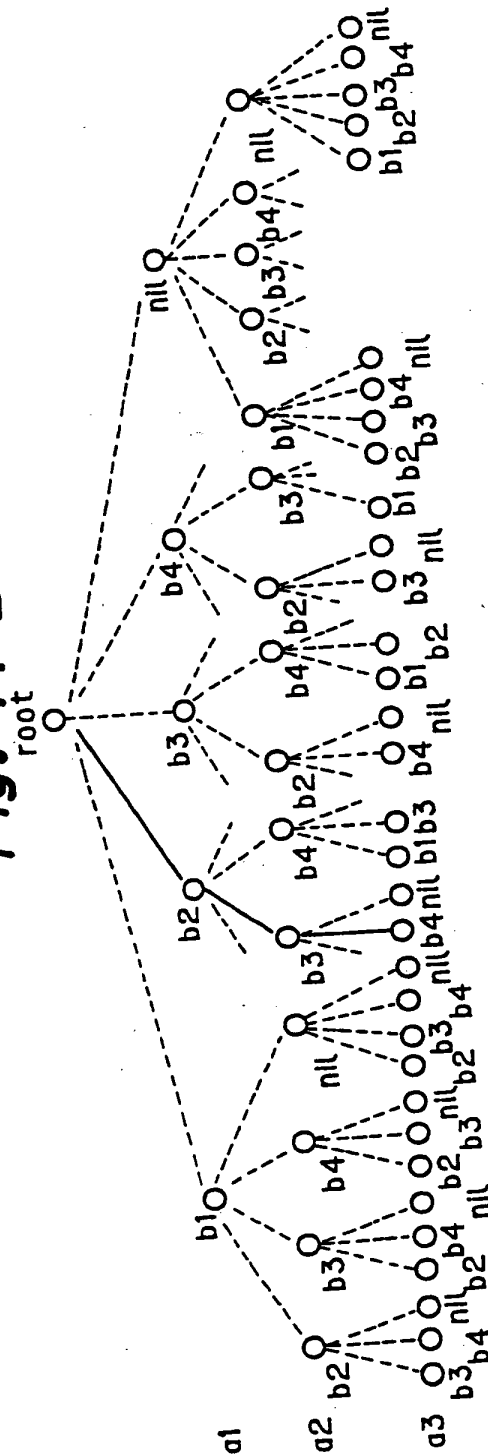
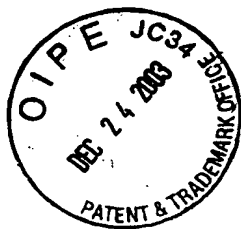
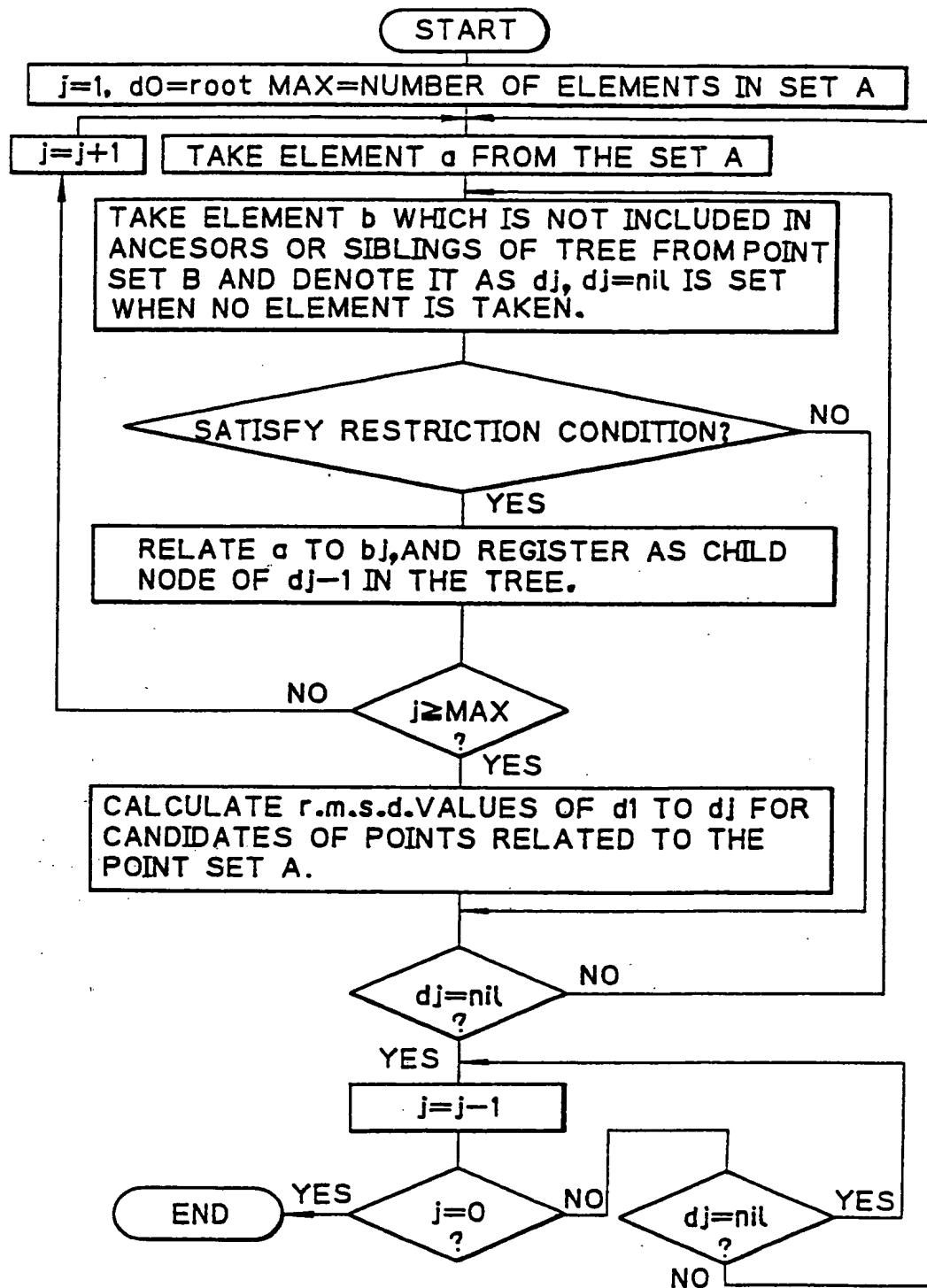


Fig. 14 B





15/45

Fig. 15

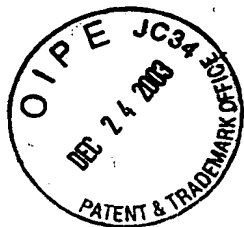


Fig. 16 A

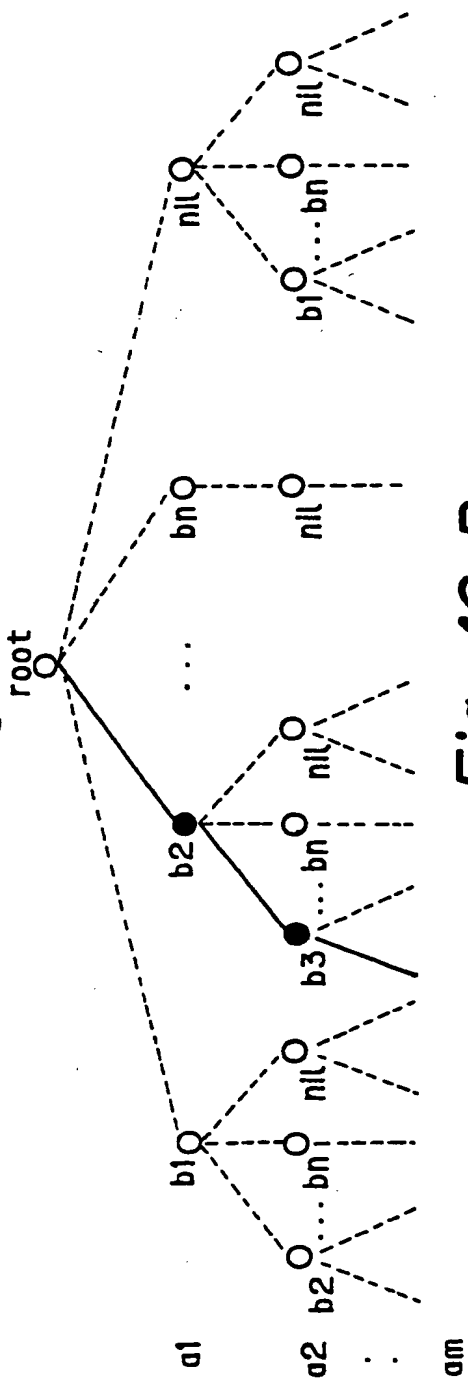
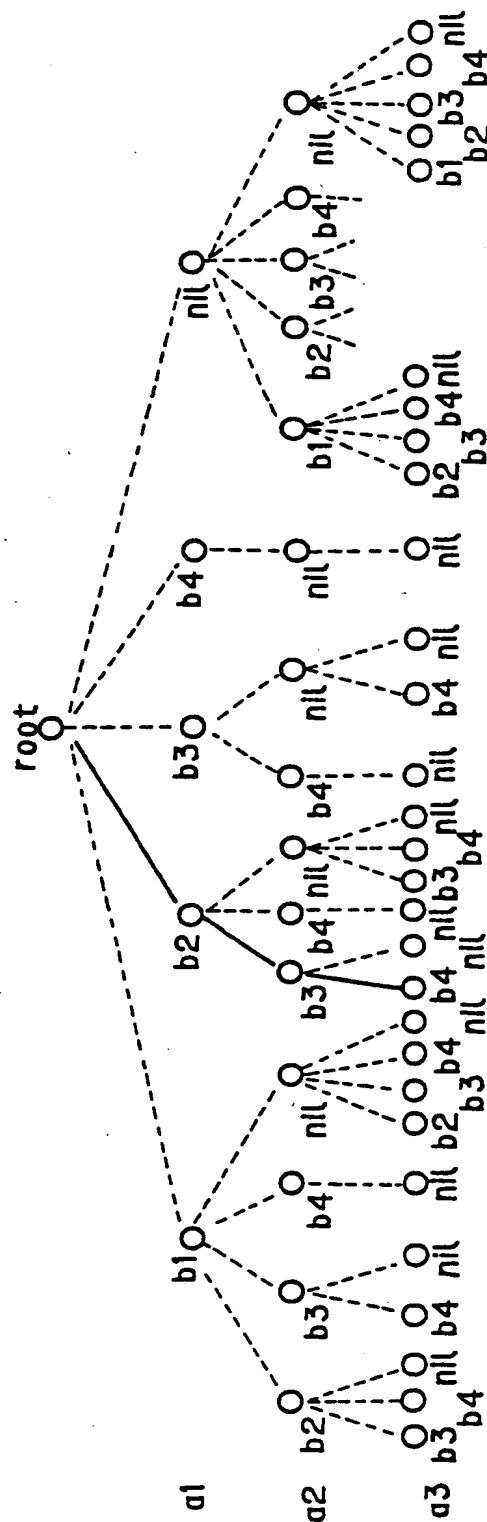
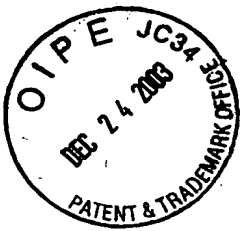
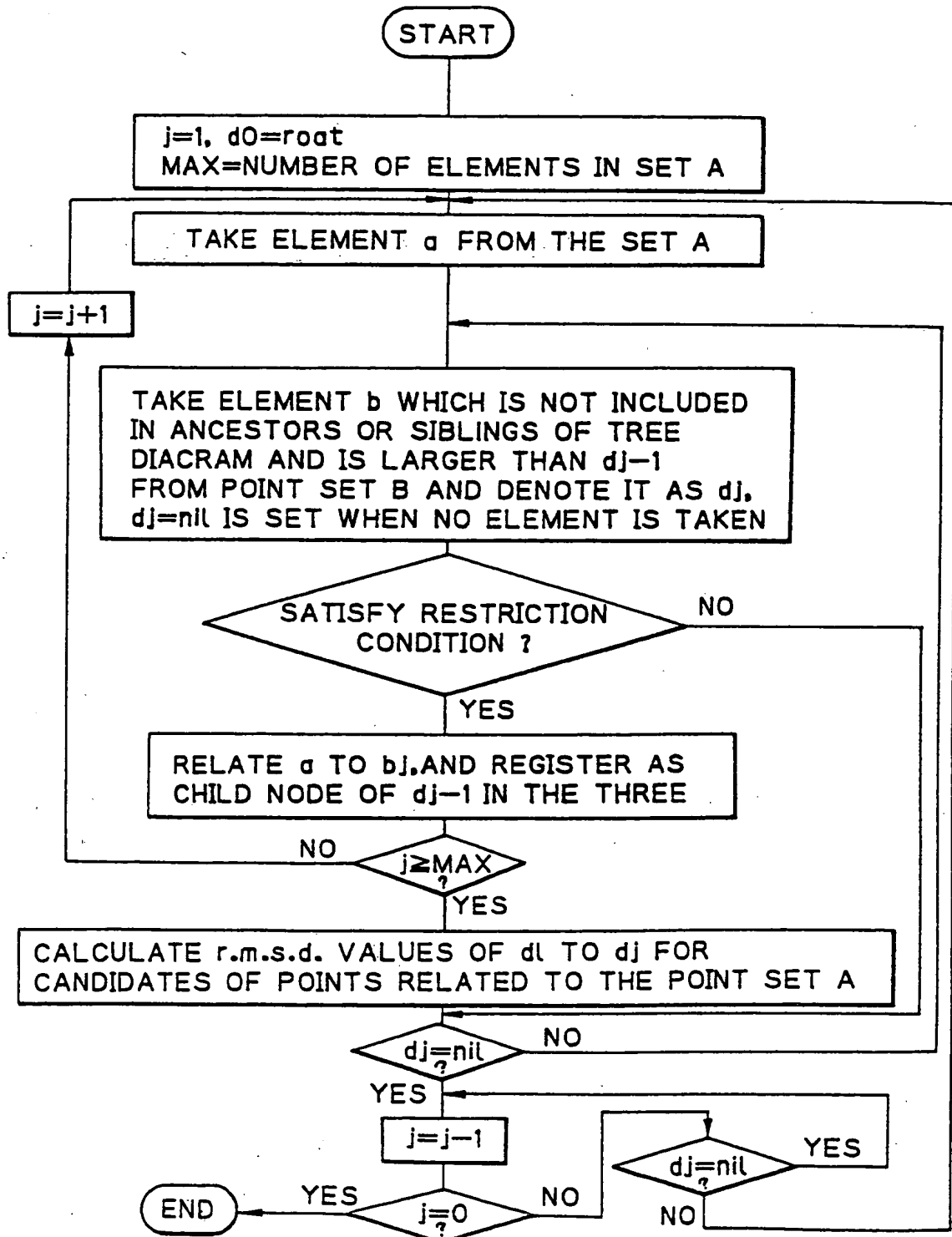


Fig. 16 B





17/45

Fig. 17

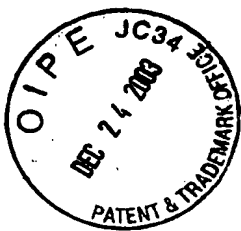
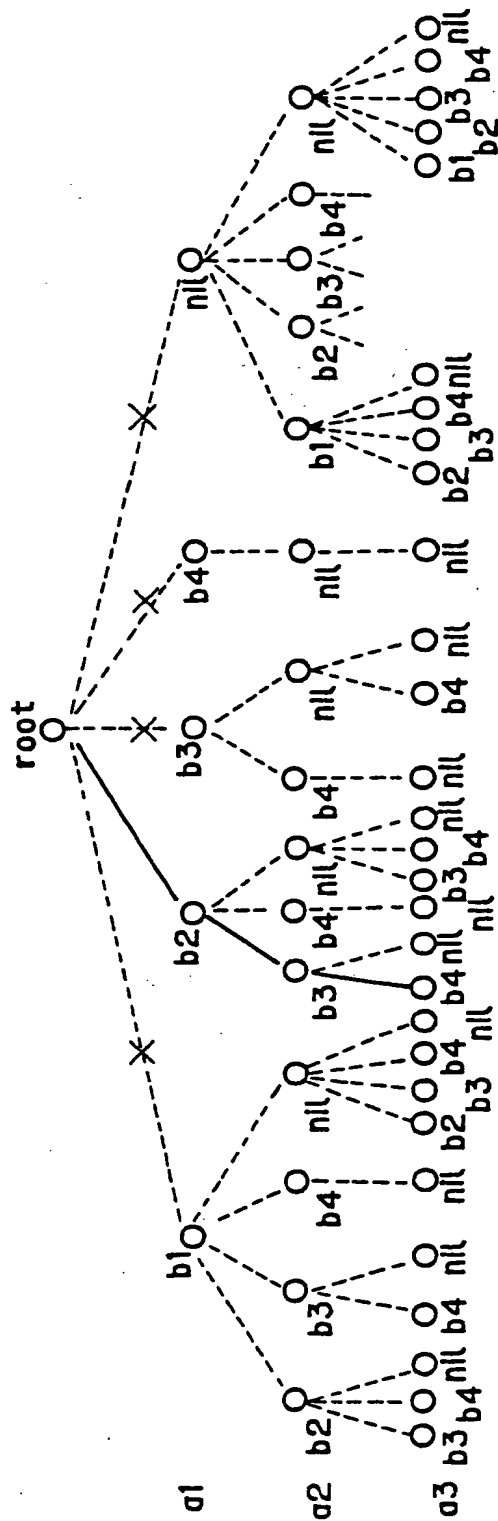
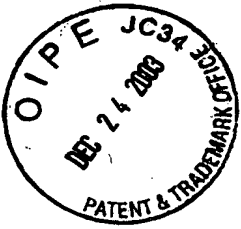


Fig. 18





19/45

Fig. 19 A

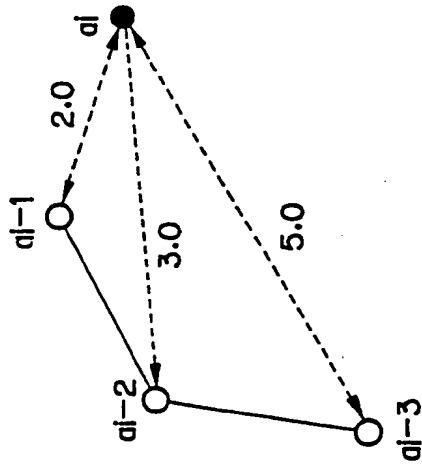


Fig. 19 B

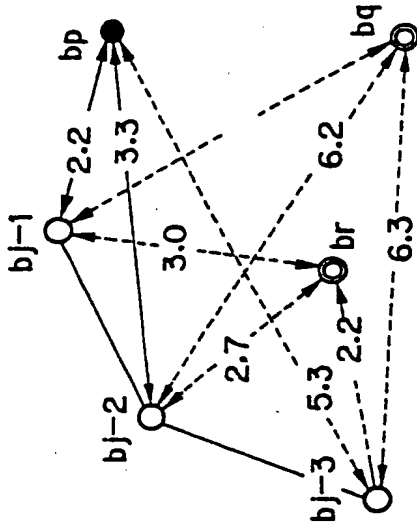


Fig. 20 A

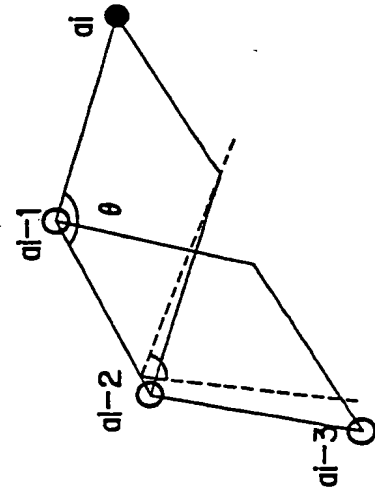
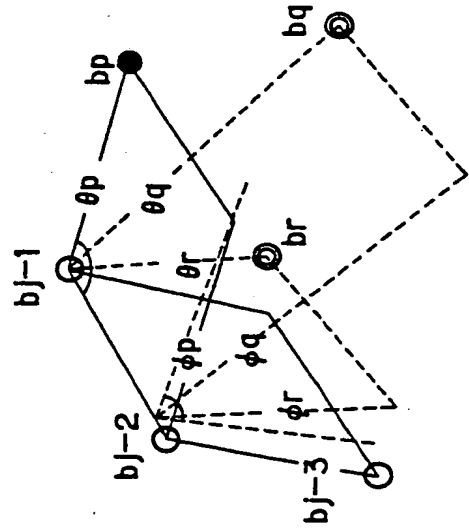
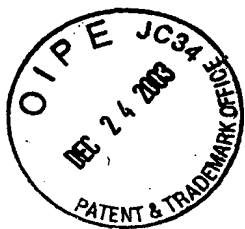


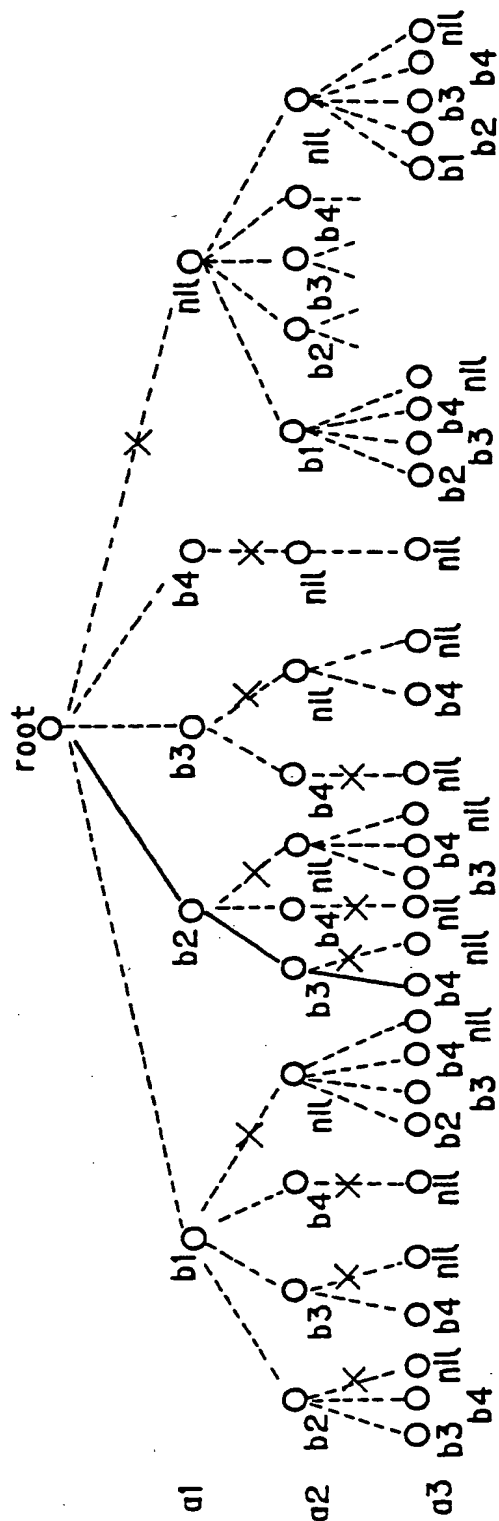
Fig. 20 B

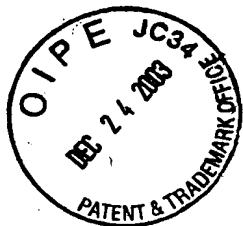




20/45

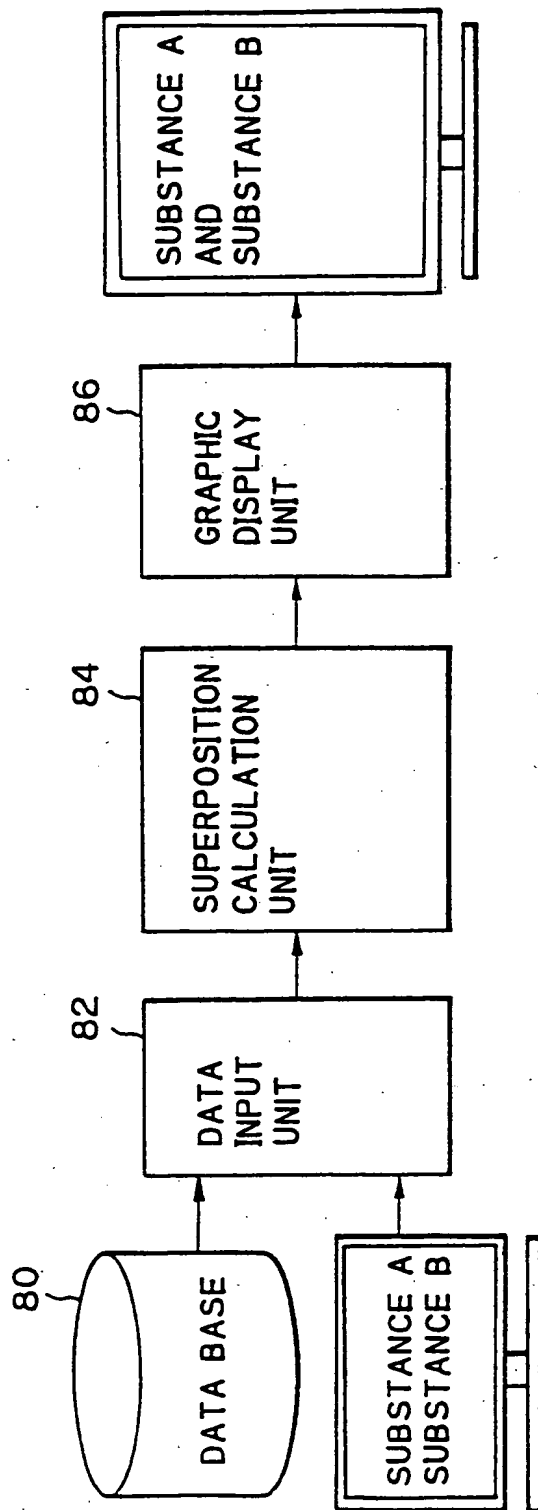
Fig. 21

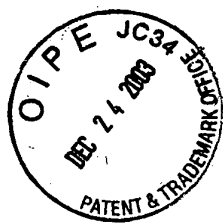




21/45

Fig. 22





22/45

Fig. 23 A

1	TEEQIAEFKE	AFSLFDKGD
21	GTITTKELGT	VMRSLGQNPT
41	EAELQDMINE	VDADGNGTID
61	FPEFLTMMAR	KMKDTDSEEE
81	IREAFRVFDK	DGNGYISAAE
101	LRHVMTNLGE	KLTDDEEVDEM
121	IREANIDGDG	QVNYEEFVQM
141	MTA	

AMINO ACID SEQUENCE OF CALMODULIN
(EXCERPT FROM PDB)

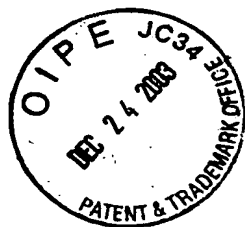
SEQ ID NO: 4

Fig. 23 B

1	AMDQQAEARA	FLSEEMIAEF
21	KAAFDMFDAD	GGDISTKEL
41	GTVMRMLGQN	PTKEELDAII
61	EEVDEDESGT	IDFEEFLVM
81	VRQMKEDAKG	KSEEELADCF
101	RIFDKNADGF	IDIEELGEIL
121	RATGEHVTEE	DIEDLMKDSD
141	KNNDGRIDFD	EFLKMMEGVQ
161		

AMINO ACID SEQUENCE OF TROPONIN C
(EXCERPT FROM PDB)

SEQ ID NO: 5



23/45

Fig. 24 B

TROPONIN C

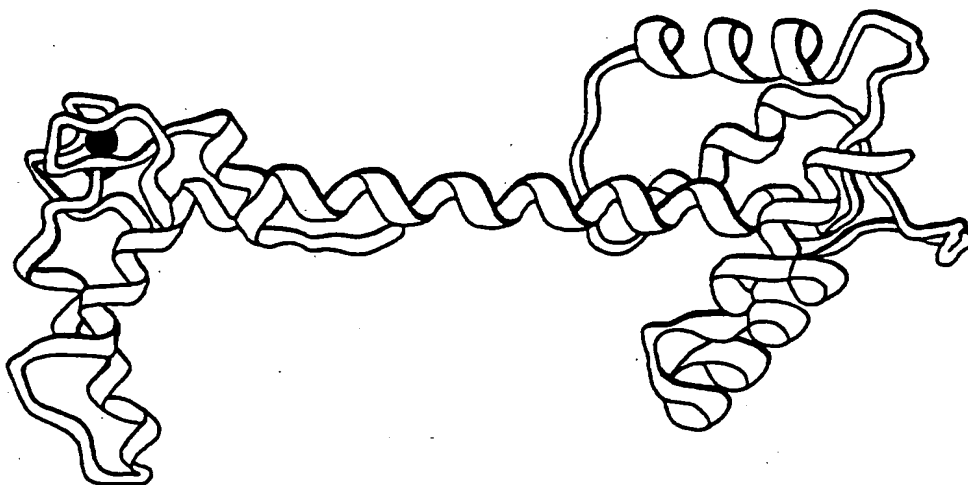
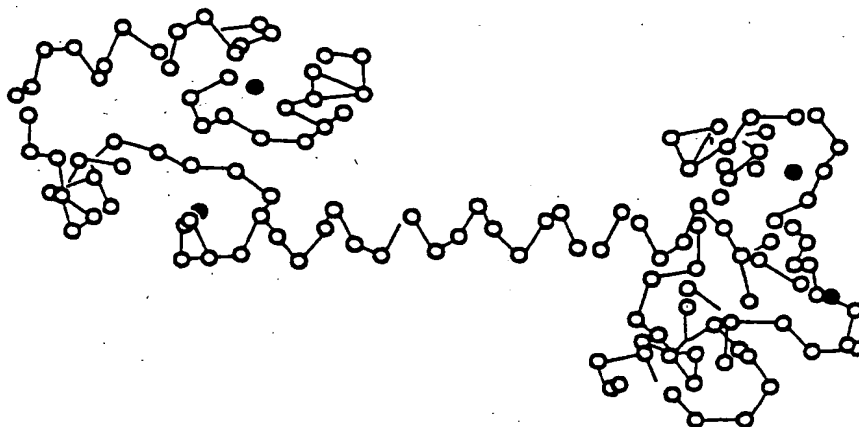
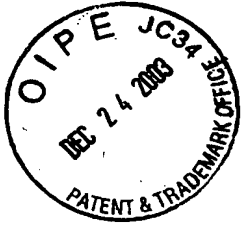


Fig. 24 A

CALMODULIN





24/45

Fig. 25

Probe site = 81-108 in Calmodulin

96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	SEQ ID NO: 6
L	A	D	C	F	R	I	F	D	K	N	A	D	G	F	< target >
I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y	< probe >
111	112	113	114	115	116	117	118	119	120	121	122	123			SEQ ID NO: 7
I	D	I	E	E	E	L	G	E	I	L	R	A	T		SEQ ID NO: 6
I	S	A	A	E	E	L	R	H	V	M	T	N	L		< target >
															< probe >
															SEQ ID NO: 7

rmsd = 0.567034



Fig. 26

Probe site = 81-108 and 117-143 in Calmodulin

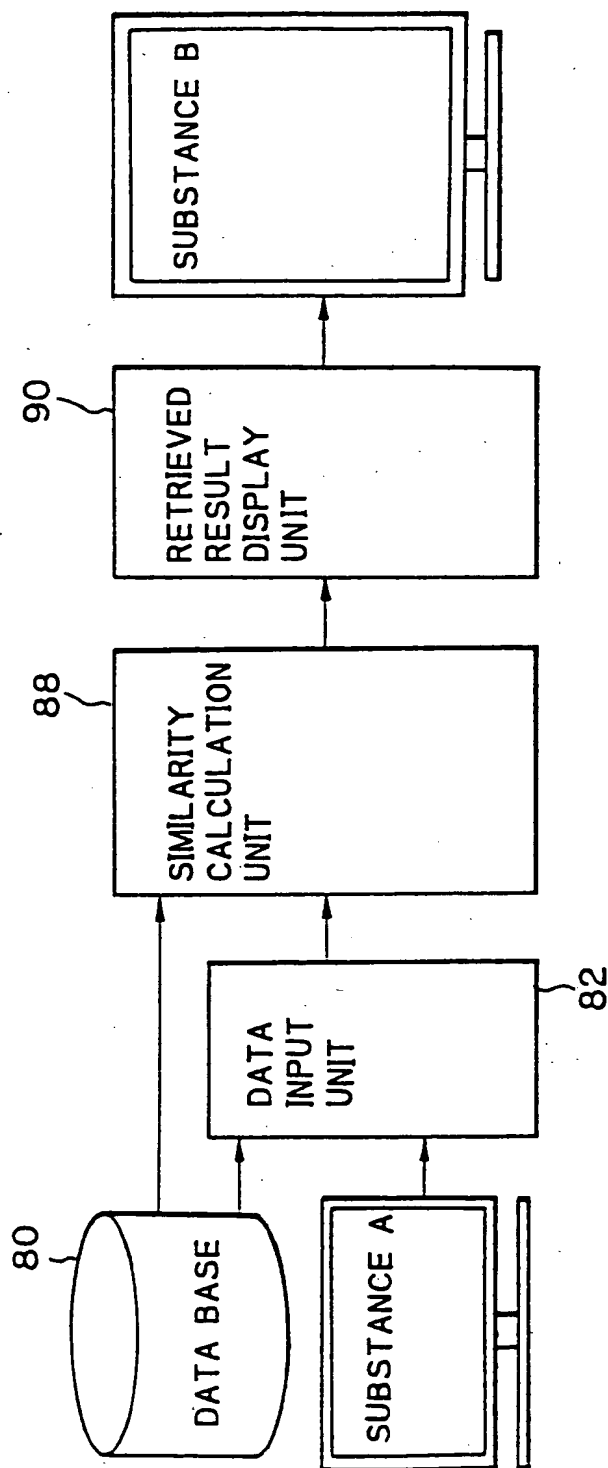
96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	SEQ ID NO: 6 < target >
L	A	D	C	F	R	I	F	D	K	N	A	D	G	F	
I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y	SEQ ID NO: 7 < probe >
111	112	113	114	115	116	117	118	119	120	121	122	123			
I	D	I	E	E	L	G	E	I	L	R	A	T			SEQ ID NO: 6 < target >
I	S	A	A	E	L	R	H	V	M	T	N	L			SEQ ID NO: 7 < probe >
132	133	134	135	136	137	138	139	140	141	142	143	144	145		
I	E	D	L	M	K	D	S	D	K	N	N	D	G		SEQ ID NO: 8 < target >
V	D	E	M	I	R	E	A	N	I	D	G	D	G		SEQ ID NO: 9 < probe >
146	147	148	149	150	151	152	153	154	155	156	157	158			
R	I	D	F	D	E	F	L	K	M	M	E	G			SEQ ID NO: 8 < target >
Q	V	N	Y	E	E	F	V	Q	M	M	T	A			SEQ ID NO: 9 < probe >

rmsd = 0.823665

26/45



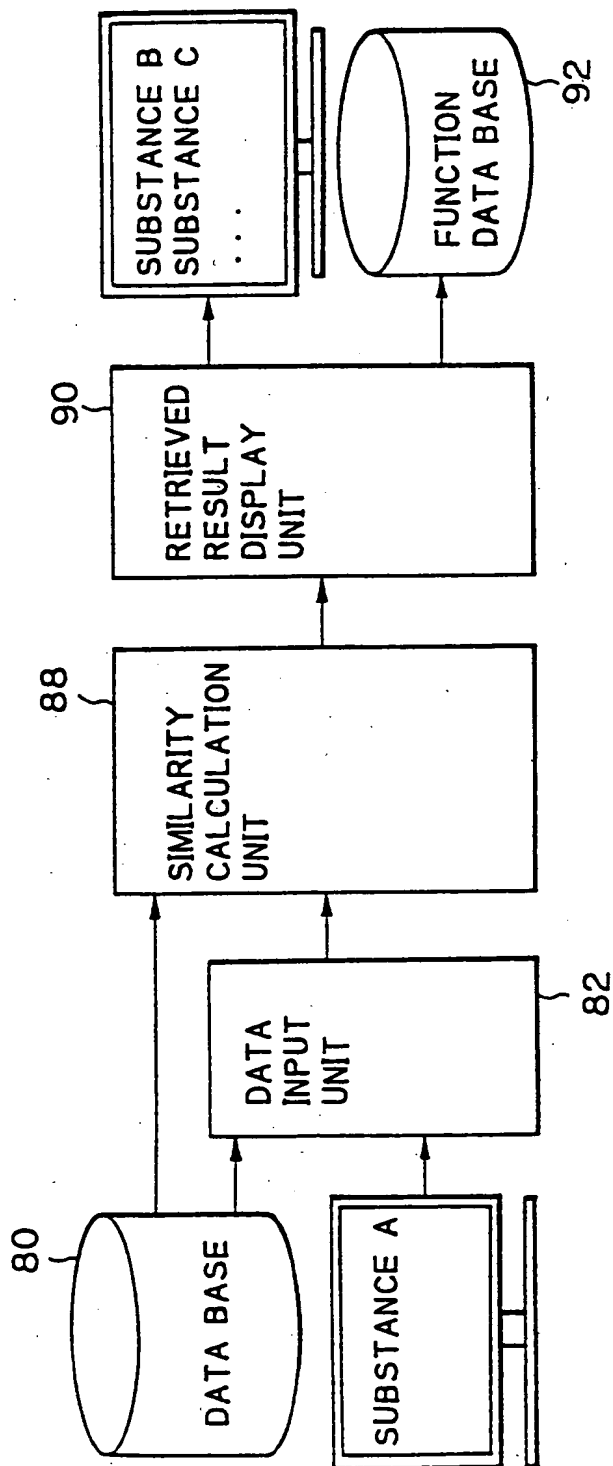
Fig. 27





27/45

Fig. 28





28/45

Fig. 29

===== ATP/GTP binding site =====

Probe = (elongation factor)

7 8 9 10 11 12 13 14
G H V D H G K T < probe > SEQ ID NO: 10

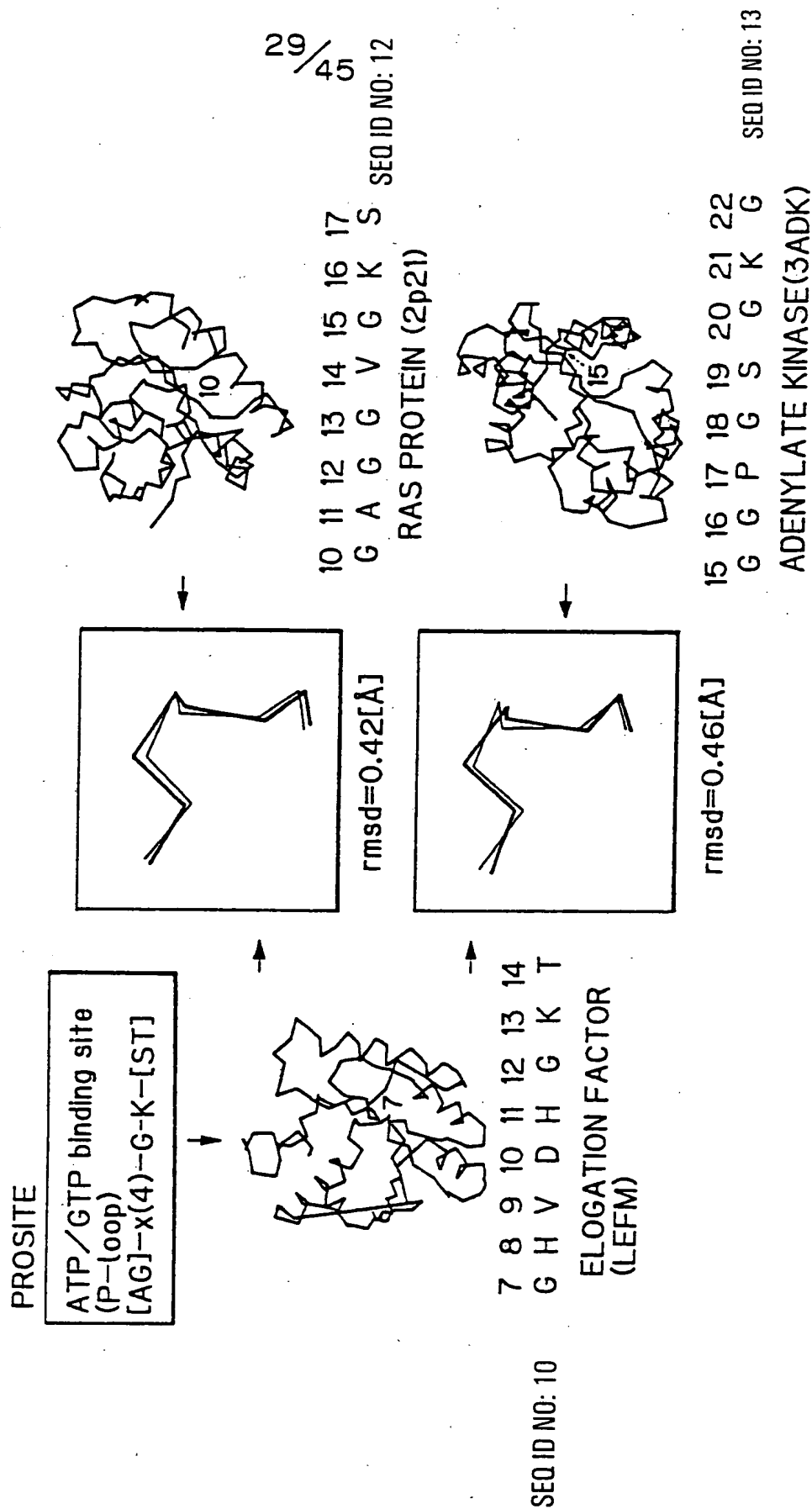
8 9 10 11 12 13 14 15
G A P G S G K G < target > SEQ ID NO: 11
G H V D H G K T < probe > SEQ ID NO: 10
rmsd=0.648732 adenylate kinase

unit - A

. : . : .
10 11 12 13 14 15 16 17
G A G G V G K S < target > SEQ ID NO: 12
G H V D H G K T < probe > SEQ ID NO: 10
rmsd=0.421770 ras protein



Fig. 30



30/45

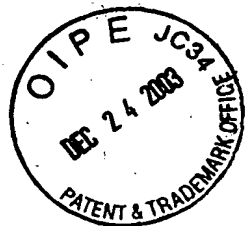
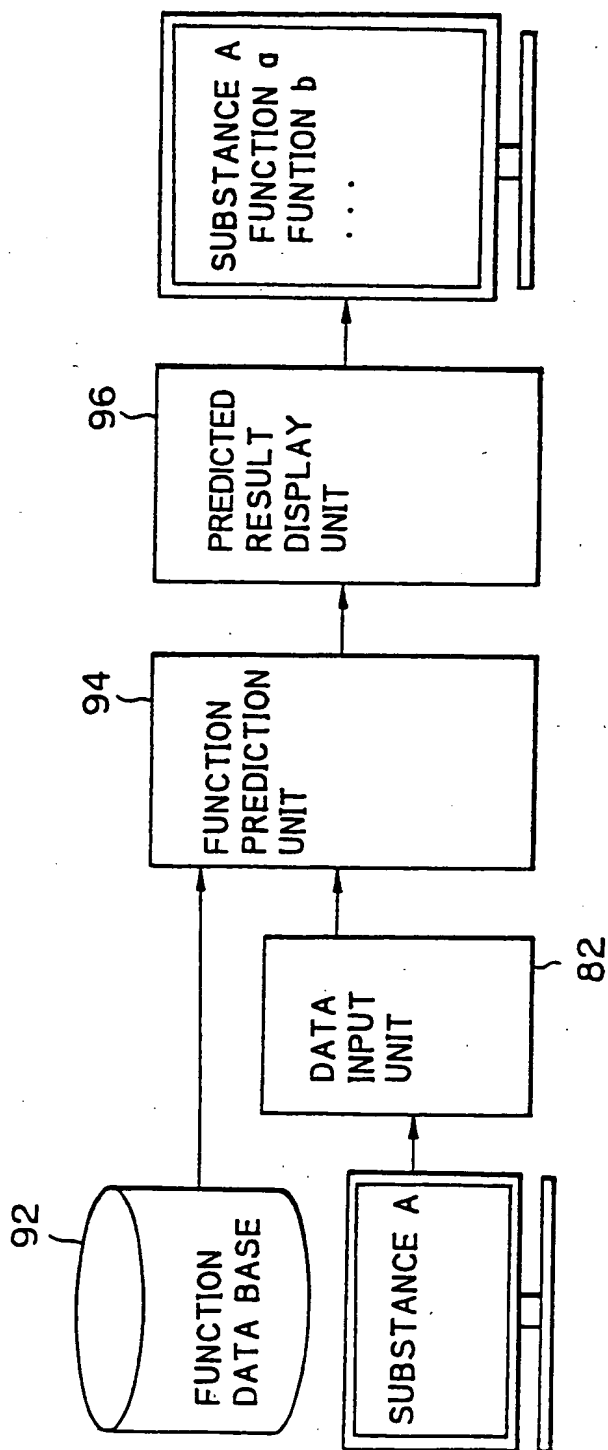
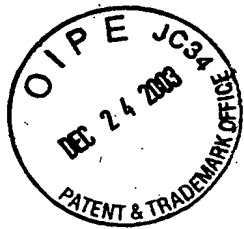


Fig. 31





31/45

Fig. 32 A

Fig. 32 B

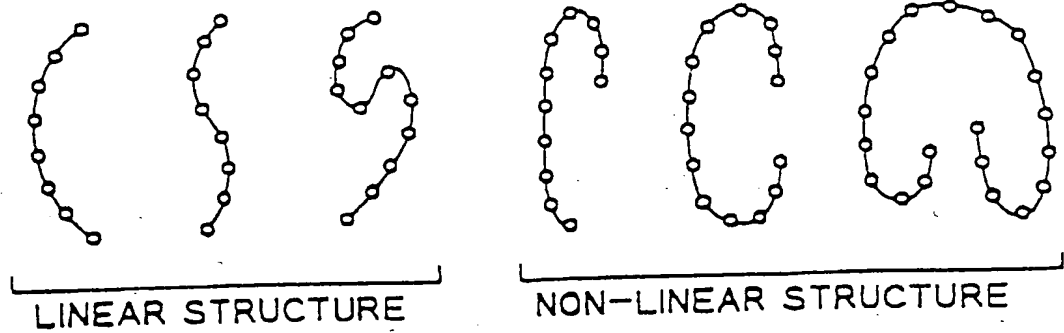
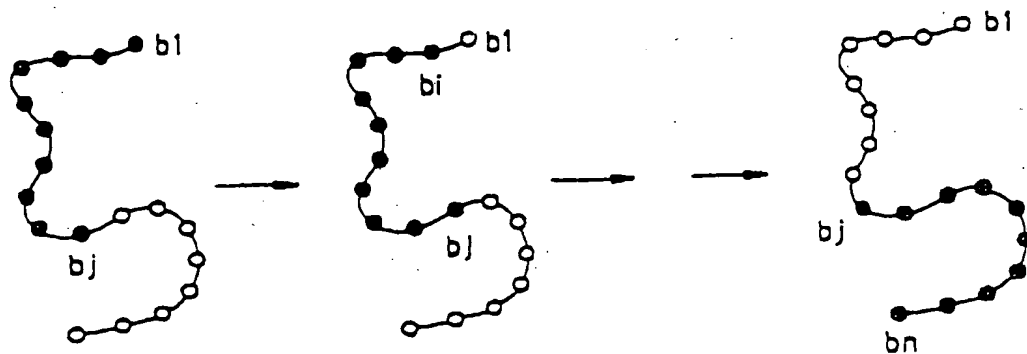


Fig. 33

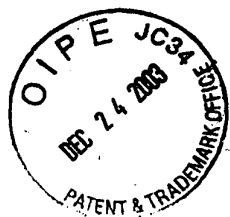
WHEN $f(x)=2x$



$A=\{a1, \dots, am\}$

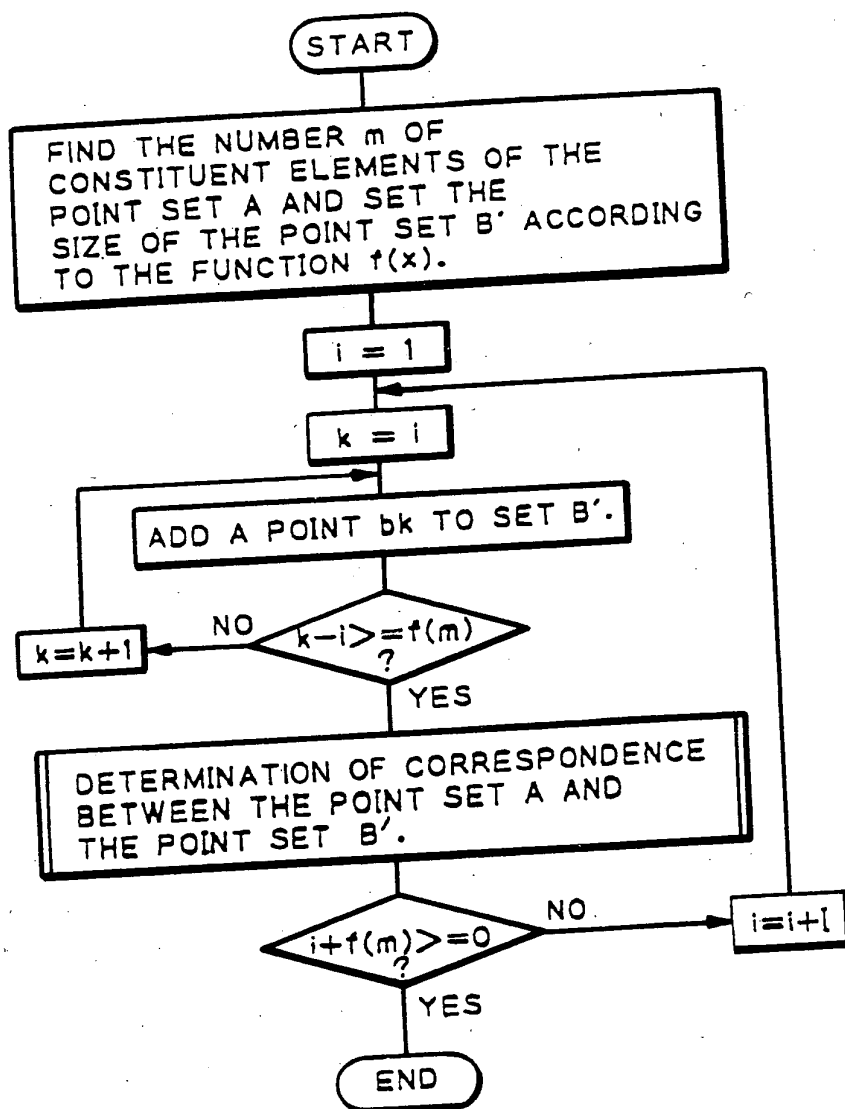


$B=\{b1, \dots, bi, \dots, bj, \dots, bn\}$



32/45

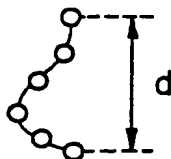
Fig. 34





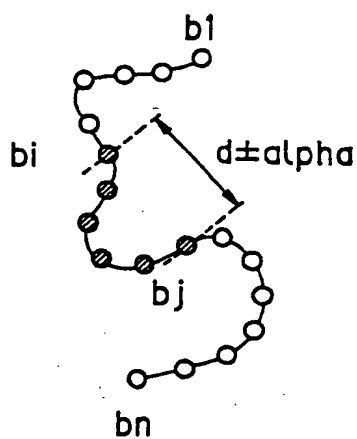
33/45

Fig. 35 A

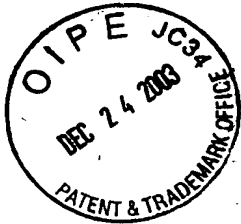


$A = \{a1, a2, \dots, am\}$

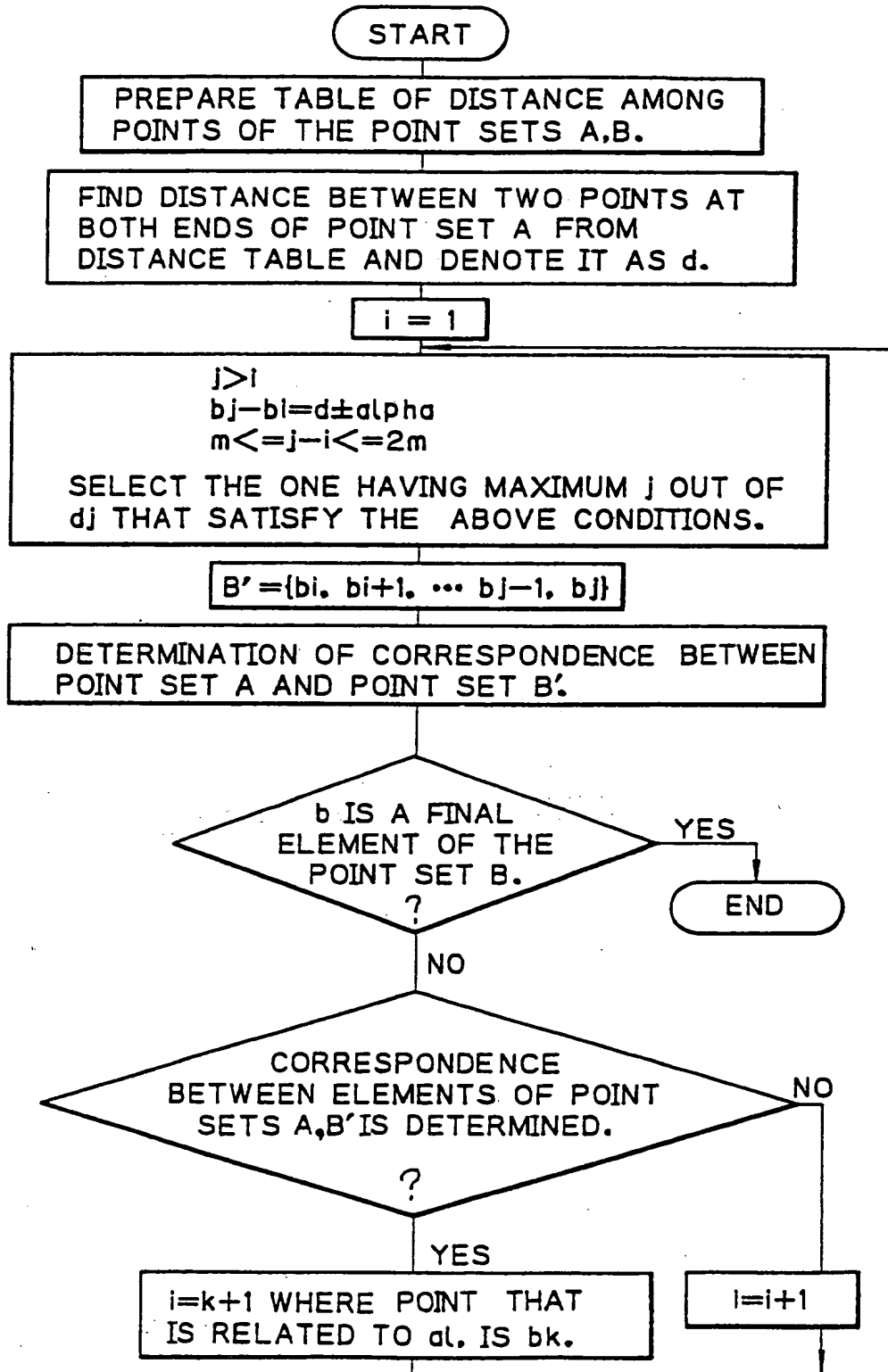
Fig. 35 B



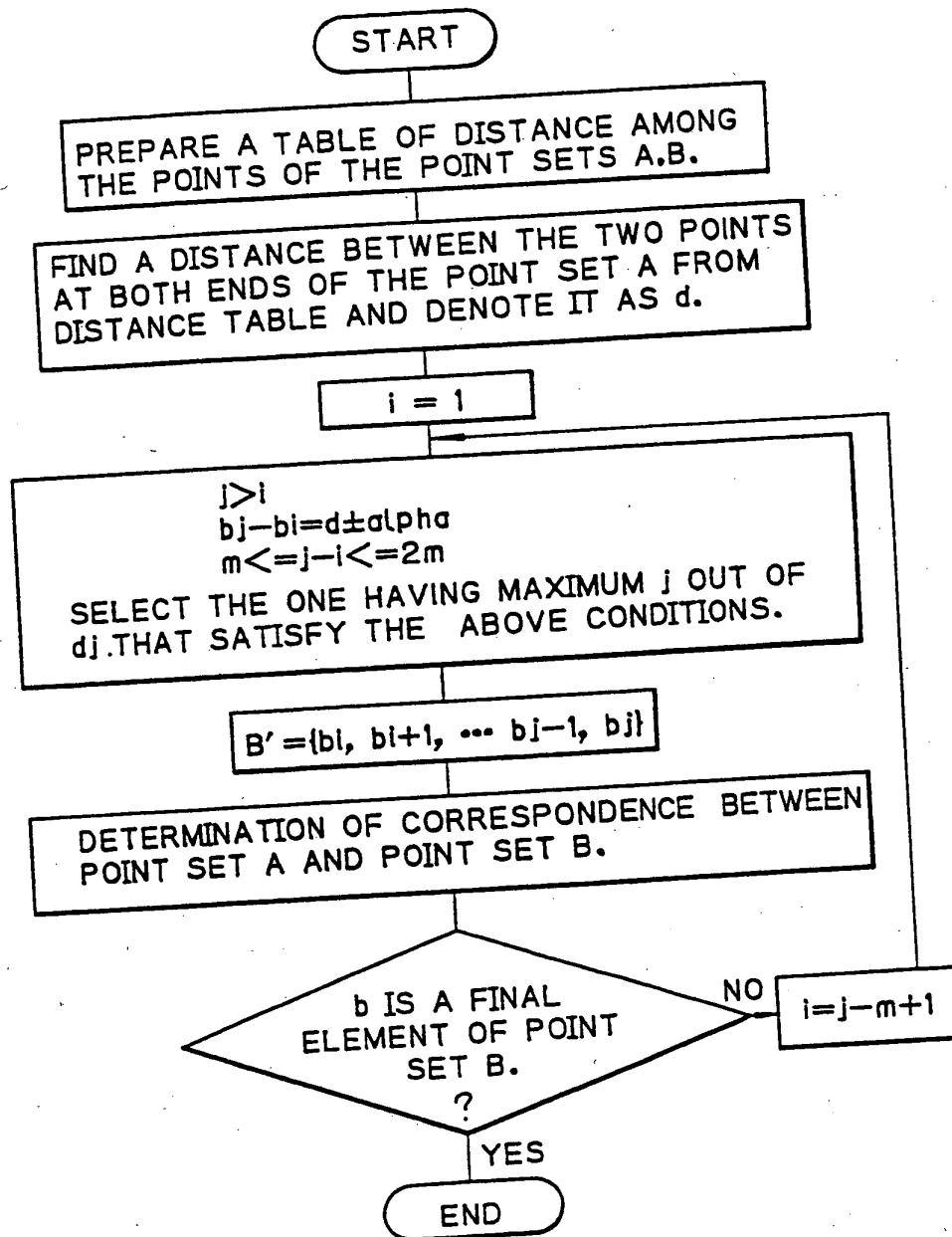
$B = \{b1, \dots, bi, \dots, bj, \dots, bn\}$



34/45

Fig. 36

35/45

**Fig. 37**



36/45

Fig. 38 A

1	I	V	G	G	Y	T	C	C	A	N	T	V	P	Y	Q	V	S	L	N	S
21	G	Y	H	F	C	G	G	S	L	I	N	S	Q	W	V	V	S	A	A	H
41	C	Y	K	S	G	I	Q	V	R	L	G	E	D	N	I	N	V	V	E	G
61	N	E	Q	F	I	S	A	S	K	S	I	V	H	P	S	Y	N	S	N	T
81	L	N	N	D	I	M	L	I	K	L	K	S	A	A	S	L	N	S	R	V
101	A	S	I	S	L	P	T	S	C	A	S	A	G	T	Q	C	L	I	S	G
121	W	G	N	T	K	S	S	G	T	S	Y	P	D	V	L	K	C	L	K	A
141	P	I	L	S	D	S	S	C	K	S	A	Y	P	G	Q	I	T	S	N	M
161	F	C	A	G	Y	L	E	G	G	K	D	S	C	Q	G	D	S	G	G	P
181	V	V	C	S	G	K	L	Q	G	I	V	S	W	G	S	G	C	A	Q	K
201	N	K	P	G	V	Y	T	K	V	C	N	Y	V	S	W	I	K	Q	T	I
221	A	S	N																	

SEQ ID NO: 14

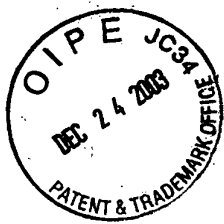
AMINO ACID SEQUENCE OF TRYPSIN (EXCERPT FROM PDB)

Fig. 38 B

1	V	V	G	G	T	E	A	Q	R	N	S	W	P	S	Q	I	S	L	Q	Y
21	R	S	G	S	S	W	A	H	T	C	G	G	T	L	I	R	Q	N	W	V
41	M	T	A	A	H	C	V	D	R	E	L	T	F	R	V	V	V	G	E	H
61	N	L	N	Q	N	N	G	T	E	Q	Y	V	G	V	Q	K	I	V	V	
81	P	Y	W	N	T	D	D	V	A	A	G	Y	D	I	A	L	L	R	L	A
101	Q	S	V	T	L	N	S	Y	V	Q	L	G	V	L	P	R	A	G	T	I
121	L	A	N	S	P	C	Y	I	T	T	G	W	G	L	T	R	T	N	G	Q
141	L	A	Q	T	L	Q	Q	A	Y	L	P	T	V	D	Y	A	I	C	S	S
161	S	S	Y	W	G	S	T	V	K	N	S	M	V	C	A	G	G	D	G	V
181	R	S	G	C	Q	G	D	S	G	G	P	L	H	C	L	V	N	G	Q	Y
201	A	V	H	G	V	T	S	F	V	S	R	L	G	C	N	V	T	R	K	P
221	T	V	F	T	R	V	S	A	Y	I	S	W	I	N	N	V	I	A	S	N

SEQ ID NO: 15

AMINO ACID SEQUENCE OF ELASTASE (EXCERPT FROM PDB)

**Fig. 39 A**

Key site number 36 - 41 in Trypsin

41	42	43	44	45	46		
M	T	A	A	H	C	< target >	SEQ ID NO: 16
V	S	A	A	H	C	< probe >	SEQ ID NO: 17

d = 12.070038 [A]

r.m.s.d. = 0.061077 [A]

The number of atoms in a probe = 6

The number of atoms in PDB = 240

The number of combination = 1

Time = 1sec

RETRIEVED RESULTS OF HISTIDINE ACTIVE SITES

Fig. 39 B

Key site number 175 - 179 in Trypsin

186	187	188	189	190		
G	D	S	G	G	< target >	SEQ ID NO: 18
G	D	S	G	G	< probe >	SEQ ID NO: 19

d = 8.922721 [A]

r.m.s.d. = 0.092879 [A]

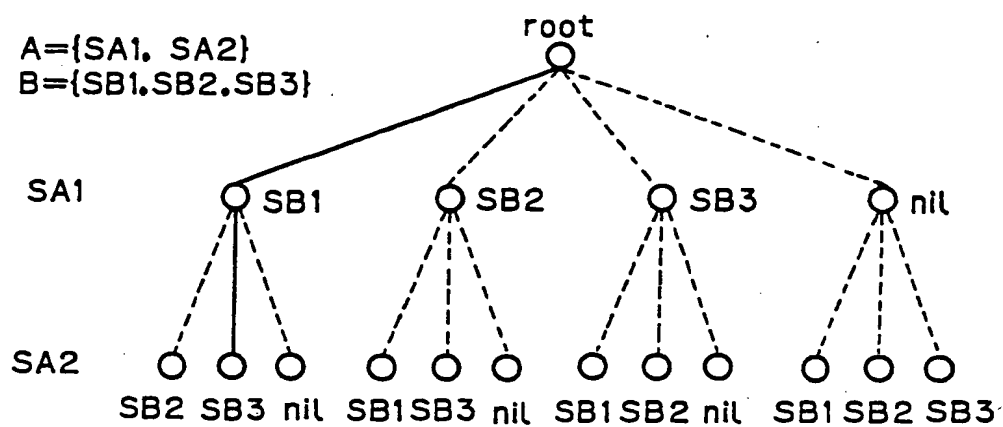
The number of atoms in a probe = 5

The number of atoms in PDB = 240

The number of combination = 1

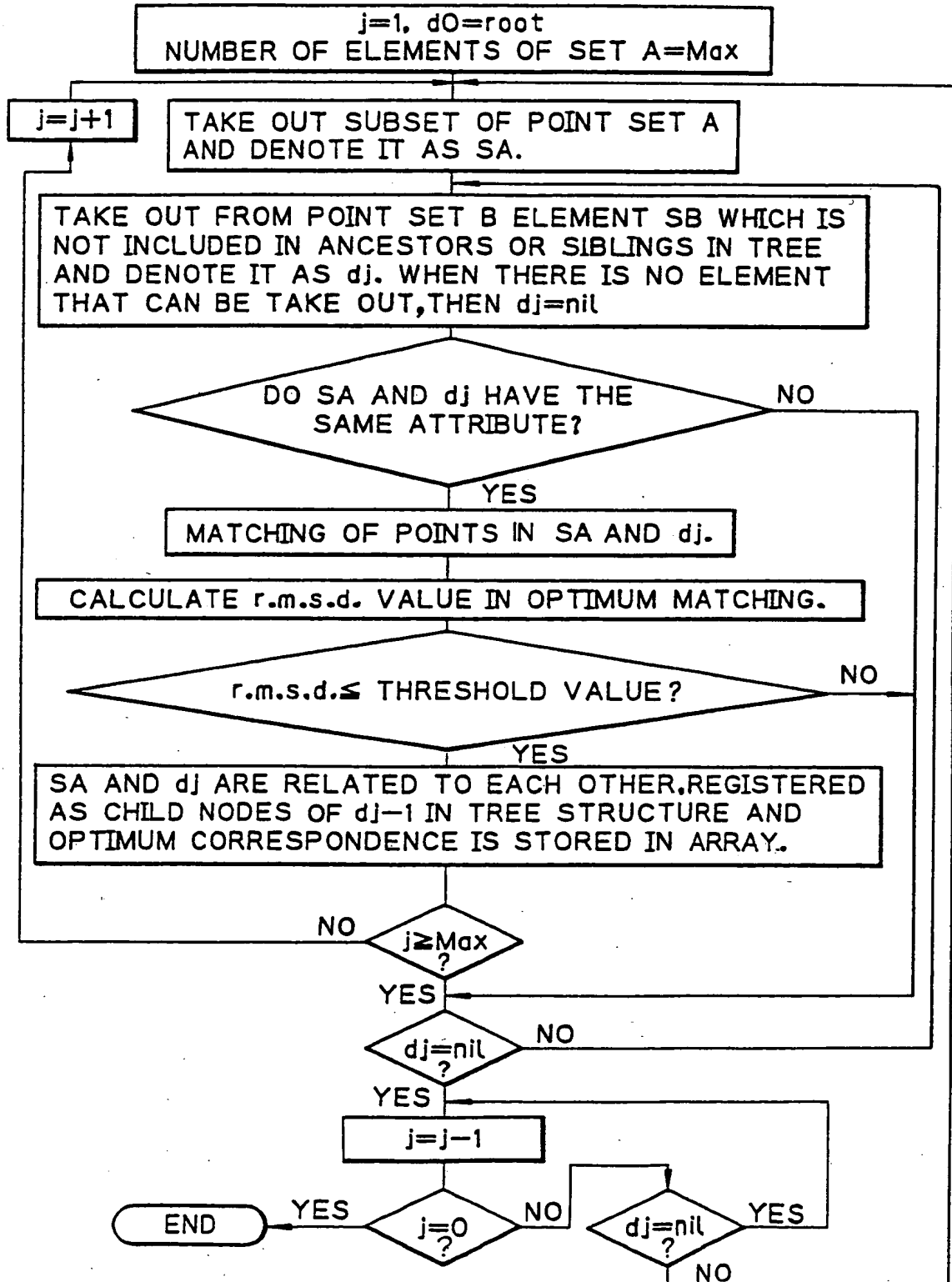
Time = 1sec

RETRIEVED RESULTS OF SERINE ACTIVE SITES

**Fig. 40**



39/45

Fig. 41

40/45

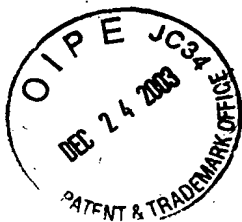
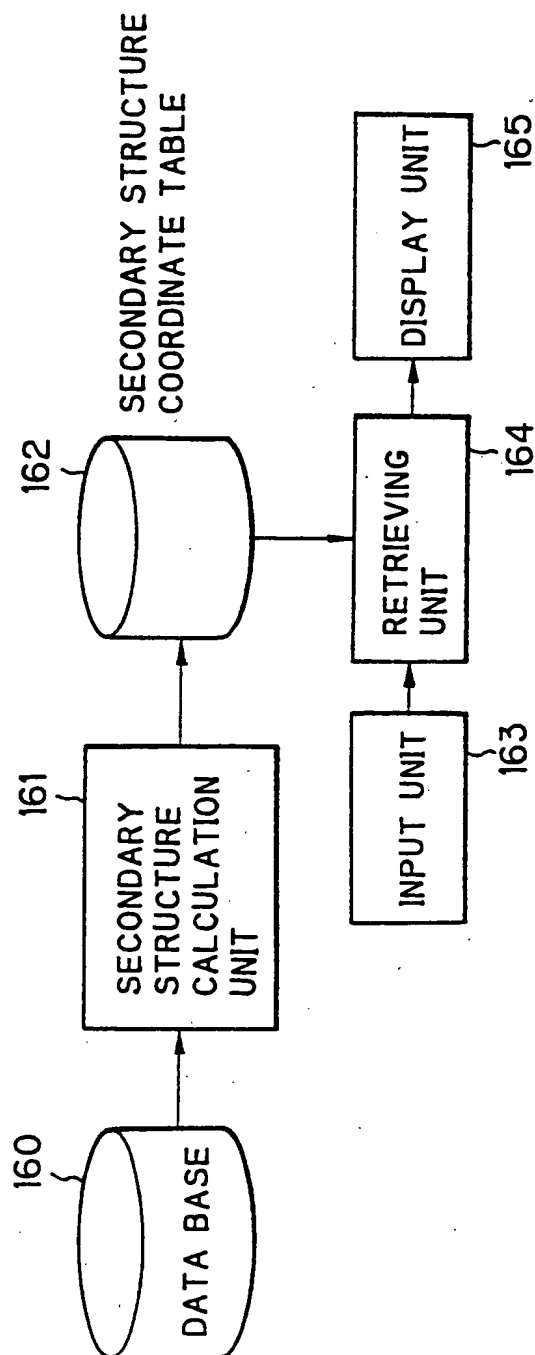
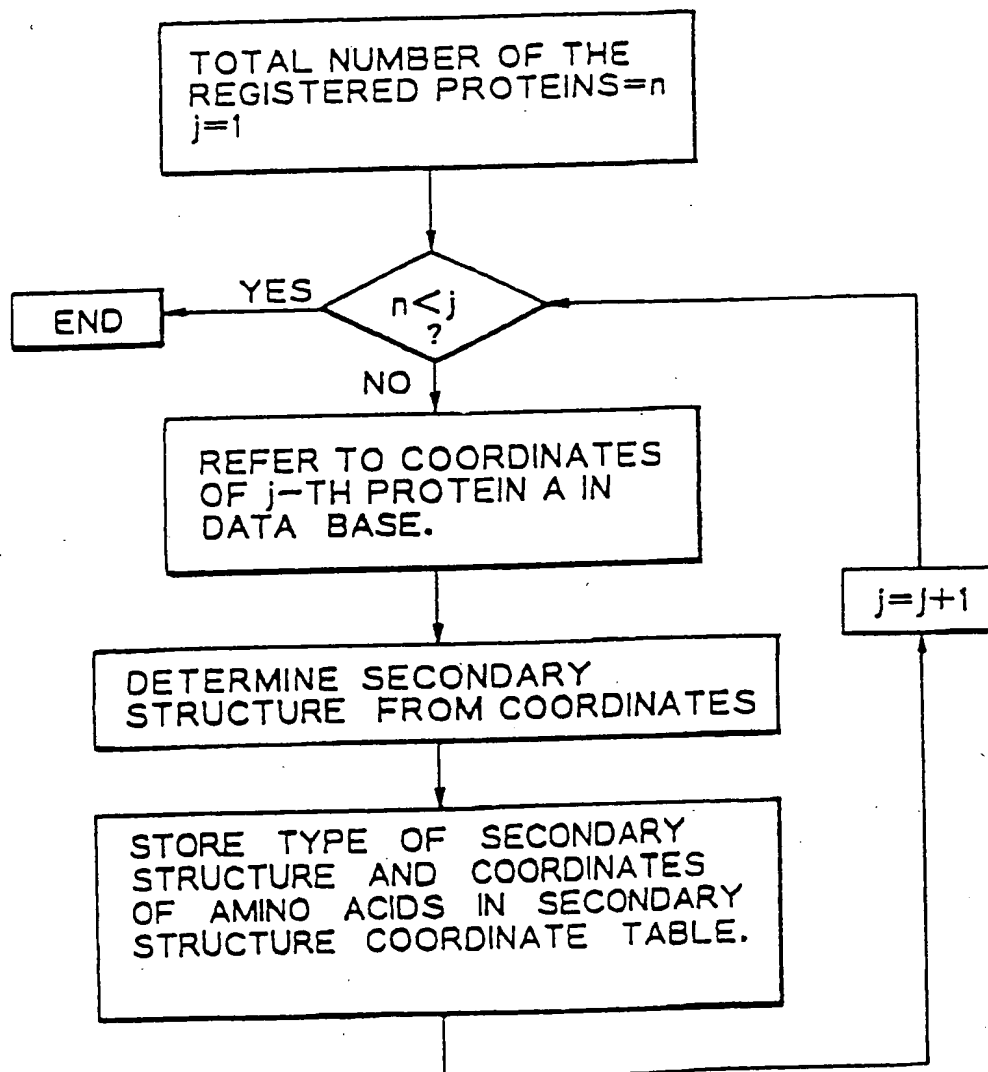
**Fig. 42**



Fig. 43



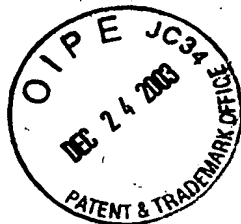


42/45

Fig. 44

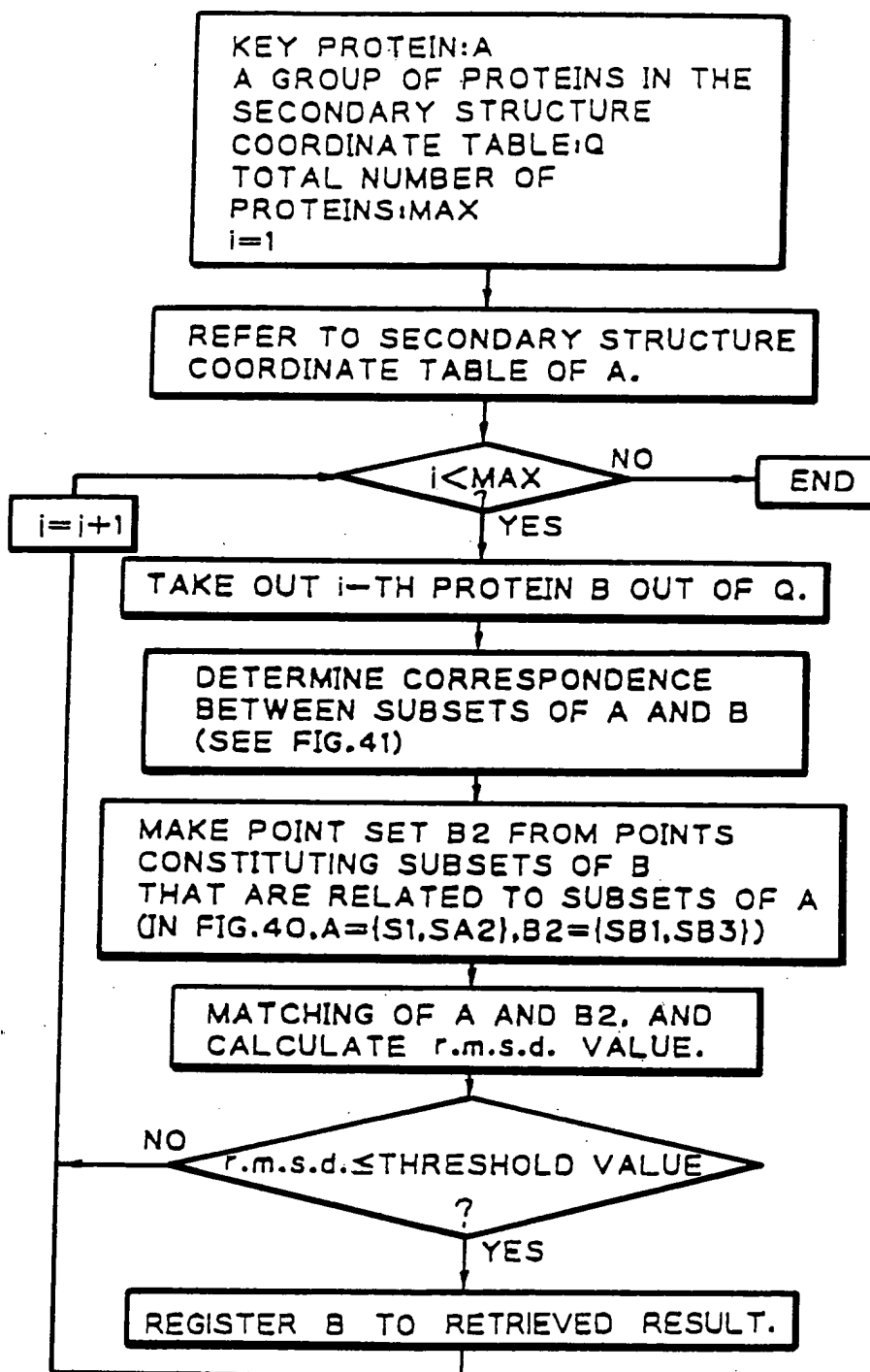
162

SUBSET	COORDINATES	TYPE
S1	{X1,X2,X3,X4,.....Xa}	α - HELIX
S2	{Xa+1,Xa+2,.....Xb}	α - HELIX
S3	{Xb+1,Xb+2,.....Xc}	β - SHEET
S4	{Xc+1,Xc+2,.....Xd}	β - SHEET
	⋮	⋮
Sn	{Xi+1,Xi+2,.....Xm}	3 - TURN



43/45

Fig. 45



44/45

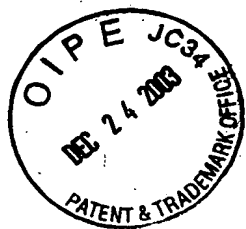
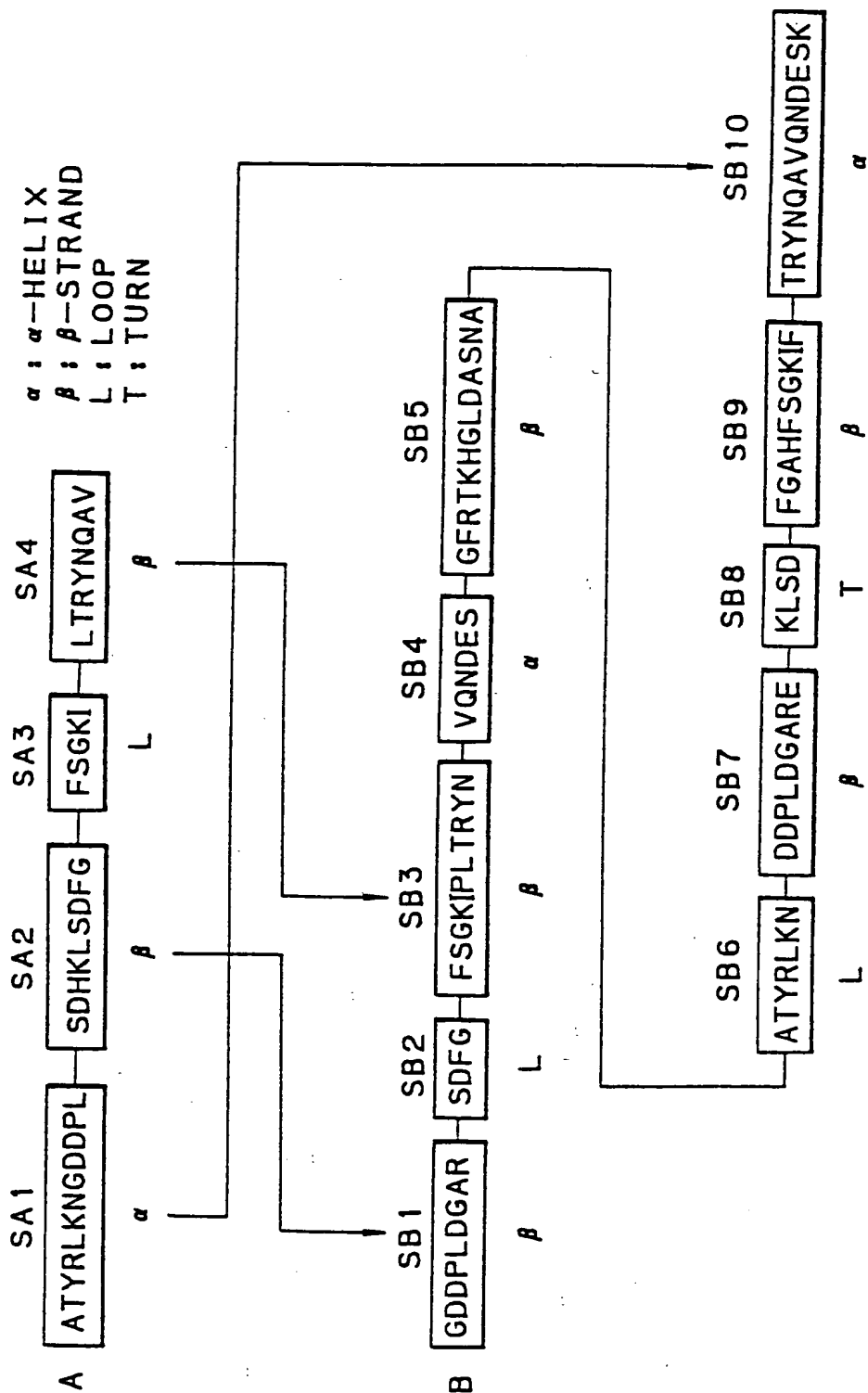


Fig. 46

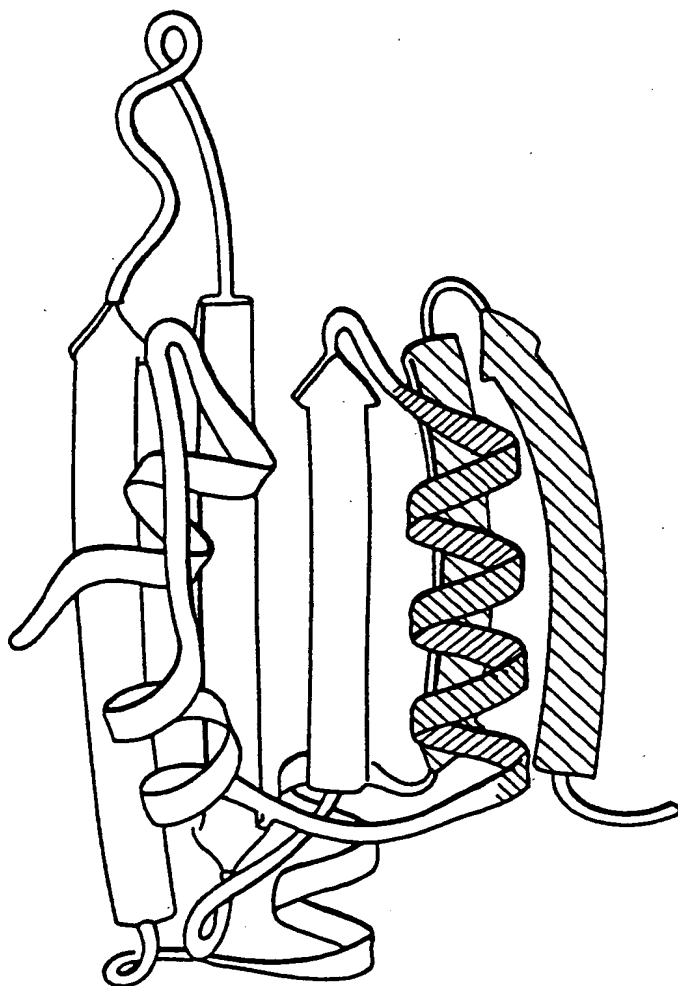


SEQ ID NO: 20



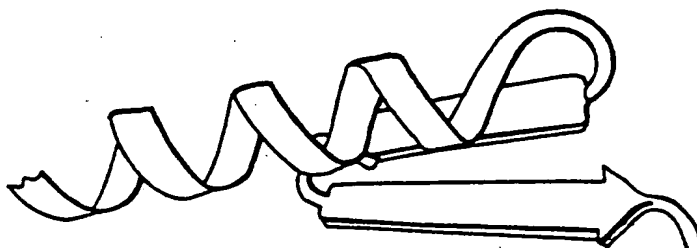
45/45

Fig. 47 B



PROTEIN B HAVING A SIMILAR STRUCTURE

Fig. 47 A



KEY PROTEIN A